

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 11:37:36 ; Search time 1160 Seconds
(without alignments)
2918.186 Million cell updates/sec

Title: US-09-600-714-41

Perfect score: 1254

Sequence: 1 atgagcttaagctaccgcg.....attgccttgatttta 1254

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1254	100.0	1254	20	AAx86522	- cDNA sequence of t
2	177	14.1	1805	24	ABK12333	cDNA encoding huma
3	175.4	14.0	1792	24	ABZ11480	Human polynucleoti
4	165.4	13.2	1853	21	AAH62486	Human membrane-ass
5	165.4	13.2	1949	22	AAH25763	Oesophagus cancer
6	165.4	13.2	1952	24	ABK49215	cDNA encoding huma
7	165.4	13.2	1968	25	ABX76257	Lung cancer-associ
8	165.4	13.2	1970	21	AAH76344	Human ORF1899

C	9	159.4	12.7	1679	24	ABK12334	cDNA encoding mous
C	10	152.4	12.2	3706	22	AAH18728	Human cDNA sequenc
C	11	150.2	12.0	2098	24	ABK49216	cDNA encoding mous
C	12	139.8	11.1	486	22	ABA42886	Human breast cell
C	13	139.8	11.1	486	22	ABA53307	Human foetal liver
C	14	139.8	11.1	486	22	ABA23081	Probe #1547 for ge
C	15	139.8	11.1	486	22	AAK01568	Human brain expres
C	16	139.8	11.1	486	22	AAK27012	Human bone marrow
C	17	139.8	11.1	486	22	AAI11615	Probe #1548 for ge
C	18	139.8	11.1	486	22	AAI32911	Probe #1597 used t
C	19	139.8	11.1	486	22	AAI01542	Probe #1533 used t
C	20	139.8	11.1	486	23	ABS26595	Human liver single
C	21	139.8	11.1	486	24	ABS01595	Human genome-deriv
C	22	120	9.6	1571	24	ABL90445	Human polynucleoti
C	23	113.8	9.1	1840	23	ABL02133	Drosophila melanog
C	24	111.8	8.9	123	22	ABA48015	Human breast cell
C	25	111.8	8.9	123	22	ABA65900	Human foetal liver
C	26	111.8	8.9	123	22	ABA32986	Probe #11452 for g
C	27	111.8	8.9	123	22	AAK14315	Human brain expres
C	28	111.8	8.9	123	22	AAK40045	Human bone marrow
C	29	111.8	8.9	123	22	AAI20829	Probe #10762 for g
C	30	111.8	8.9	123	22	AAI46064	Probe #14750 used
C	31	111.8	8.9	123	22	AAI06540	Probe #6531 used t
C	32	111.8	8.9	123	23	ABS39627	Human liver single
C	33	111.8	8.9	123	24	ABS14127	Human genome-deriv
C	34	109.6	8.7	1650	21	AAZ97083	Human secreted pro
C	35	108.6	8.7	484	22	AAI90968	Human polynucleoti
C	36	108.6	8.7	16918	24	ABL33617	Human immune syste
C	37	101.2	8.1	1765	24	AAH28951	Human MOLT CDNA.
C	38	93.2	7.4	1222	22	AAH98147	Human EST-derived
C	39	82.2	6.6	16918	24	ABL33616	Human immune syste
C	40	79.2	6.3	730	22	AAH31425	Human secreted pro
C	41	79.2	6.3	730	24	ABL90632	Human polynucleoti
C	42	61.2	4.9	198	24	ABN75889	Human glycoprotein
C	43	57	4.5	449	22	AAH93284	cDNA encoding SRT
C	44	56.6	4.5	446	22	ABA50433	Human breast cell
C	45	56.6	4.5	446	22	ABA68382	Human foetal liver

ALIGNMENTS

RESULT 1	AAx86522	standard; cDNA: 1254 BP.
ID	AAx86522	
AC	AAx86522;	
XX		
DT	04-OCT-1999	(first entry)
XX		
DE	cDNA sequence of the prevalent allele of the Rhd gene.	
XX		
KW	Allele; Rhesus D antigen; RHD; weak D phenotype; blood transfusion; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..1254
FT		/+tag- a
XX		
PN	W09937763-A2.	
XX		
PD	29-JUL-1999.	
XX		
PF	18-DEC-1998;	98MO-EP08319.
XX		
PR	23-JAN-1998;	98BP-0101203.
XX		
PA	(DRKB-) DRK BLUTSPENDEDIENST BADEN WUERTTEMBERG.	
XX		
PI	Flegel WA, Wagner FF;	
XX		
DR	WPI; 1999-469127/39.	

DR P-PSDB: AA124056.
 XX Nucleic acid sequences correlated with Rhesus weak D phenotype.
 PT Useful for screening blood from donors and recipients for
 PT transfusion methods
 XX
 PS Disclosure: Fig 2; 64pp; English.
 XX
 CC The present sequence represents the prevalent allele of the Rhesus D
 CC (Rhd) antigen gene. The specification describes a Rhd contributing to
 CC or indicative of the weak D phenotype, where the Rhd polynucleotide
 CC carries at least one missense mutation as compared to the wild-type Rhd,
 CC in its transmembrane and/or intracellular regions, especially in amino
 CC acid positions 2-16, 114-149, 179-225 or/and 267-397, with the proviso
 CC that the D antigen does not carry a single missense mutation leading to
 CC a F223V or T283I substitution. The probes and antibodies are useful in
 CC the methods for detection of weak D phenotypes. Red blood cells, from
 CC probands, are useful for the assessment of the affinity, avidity and/or
 CC reactivity of monoclonal anti-D antibodies, polyclonal anti-D antisera or
 CC of anti-globulin or anti-human-globulin antisera. Detecting the presence
 CC of the Rhd associated with weak D phenotype is useful for determining
 CC that a patient in need of a blood transfusion is to be transfused with
 CC RhD negative blood from a donor. Alternatively, testing for weak D
 CC phenotype Rhd in the blood of a donor is useful for determining whether
 CC the donor blood should be excluded for transfusion to patients having
 CC wild type Rhd or weak D types, other than that of the donor weak D
 CC type.
 CC
 XX
 SQ Sequence 1254 BP; 241 A; 322 C; 351 G; 340 T; 0 other;
 Query Match 100.0%; Score 1254; DB 20; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 601 ACAGCAAGATACCAAGTTTGTCTGCCATGCTGGGCGCCCTCTTCTTGATGATTTCTGG 660
 DB 601 ACAGCAAGATACCAAGTTTGTCTGCCATGCTGGGCGCCCTCTTCTTGATGATTTCTGG 660
 QY 661 CCAAGTTTCAACTCTGCTCTGCTGAGAACTCCAAATGGAAGAATGCCGTGTTCAAC 720
 DB 661 CCAAGTTTCAACTCTGCTCTGCTGAGAACTCCAAATGGAAGAATGCCGTGTTCAAC 720
 QY 721 ACCATGATGCTGTAGACAGTACGCTGGTGGACAGCCATCTCAGGGATCATCCTTGGGTCAC 780
 DB 721 ACCATGATGCTGTAGACAGTACGCTGGTGGACAGCCATCTCAGGGATCATCCTTGGGTCAC 780
 QY 781 CCCCAAGGAAGATCAGCAAGACTTATGTGCACAGTCCGCTGTTGGCAGAGGCGTGGCT 840
 DB 781 CCCCAAGGAAGATCAGCAAGACTTATGTGCACAGTCCGCTGTTGGCAGAGGCGTGGCT 840
 QY 841 GTGGGATACCTCGGTGATCACTGATCCCTTCCCTGGCTGGCCATGCTGCTGGGCTCTTGG 900
 DB 841 GTGGGATACCTCGGTGATCACTGATCCCTTCCCTGGCTGGCCATGCTGCTGGGCTCTTGG 900
 QY 901 GCTGGCTGATCTCCGTCGGGAGGCCAAGTACCTCCGAGGCTGTTAAACGAGTGTG 960
 DB 901 GCTGGCTGATCTCCGTCGGGAGGCCAAGTACCTCCGAGGCTGTTAAACGAGTGTG 960
 QY 961 GGGATTCGCCACAGCTCCATCATGAGGCTACACACTTACGTTGCTGGGCTCTGTTGAGAG 1020
 DB 961 GGGATTCGCCACAGCTCCATCATGAGGCTACACACTTACGTTGCTGGGCTCTGTTGAGAG 1020
 QY 1021 ATCATCTACATGTTGGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1080
 DB 1021 ATCATCTACATGTTGGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1080
 QY 1081 TTCCAGGCTCCTCCTCAGCATTTGGGGAACCTGAGTGGCCATCTGATAGCTCTCAGCTGT 1140
 DB 1081 TTCCAGGCTCCTCCTCAGCATTTGGGGAACCTGAGTGGCCATCTGATAGCTCTCAGCTGT 1140
 QY 1141 GGTCTCCTGACAGGTTTGTCTCTAAATCTTAAATATGGAAGACACCTCATGAGGCTTAA 1200
 DB 1141 GGTCTCCTGACAGGTTTGTCTCTAAATCTTAAATATGGAAGACACCTCATGAGGCTTAA 1200
 QY 1201 TATTGTGATGACCAAGTTTCTGGAAGTTTCCATTTGGCTGTGGATTTTAA 1254
 DB 1201 TATTGTGATGACCAAGTTTCTGGAAGTTTCCATTTGGCTGTGGATTTTAA 1254

RESULT 2
 ABK12333
 ID ABK12333 standard; cDNA; 1805 BP.
 XX
 AC ABK12333;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE cDNA encoding human nonerythroid Rh glycoprotein RhBG.
 XX
 KW Human: nonerythroid Rh glycoprotein; Rhbg; RhBG; antibody; immunogen;
 KW Rh type B transporter gene; polytypic transporter-type protein;
 KW ion transporter; chromosome 1q21.3; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 39..1415
 FT /tag= a
 FT /product= "Human RhBG protein"
 FT misc_feature 1248..1377
 FT /tag= b
 FT /note= "Encodes C-tail"
 FT polyA_signal 1769..1774
 FT /tag= c
 FT /note= "PolyA signal"
 FT /note= "Atypical polyadenylation site"

XX WO200216396-A2.
 PN
 XX 28-FEB-2002.
 PD
 XX 17-AUG-2001; 2001WO-US25881.
 PF
 XX 21-AUG-2000; 2000US-226767P.
 PR
 XX (NYBL-) NEW YORK BLOOD CENT INC.
 PA
 XX Huang C, Liu Z;
 PI
 XX WPI: 2002-280905/32.
 DR P-PSDB; AAU78091.
 XX
 PT Homologues of mouse or human nonerythroid Rh glycoproteins, Rhbg or Rhbg,
 PT respectively, useful in the production of antibodies which are useful
 PT for detecting Rhbg or Rhbg glycoproteins in a sample -
 PS
 XX Claim 1; Fig 1a; 59pp; English.
 CC The present invention relates to a new protein or peptide comprising an
 CC amino acid sequence having at least 60% identity to a sequence comprising
 CC 455 (mouse nonerythroid Rh glycoprotein homologue (Rhbg)) or 458 (human
 CC nonerythroid Rh glycoprotein homologue (Rhbg)) amino acids, fully defined
 CC in the specification. The antibody of the invention is useful for
 CC detecting an Rhbg or an Rhbg glycoprotein in a sample, by contacting the
 CC sample with antibody under conditions suitable for binding, assessing the
 CC specific binding to the antibody, and thus detecting the presence of an
 CC epitope of Rhbg or Rhbg in the sample. The nucleic acids of the invention
 CC are useful as probes for detecting transporter genes and particularly Rh
 CC type B transporter genes including e.g. NH₄⁺ ion transporters. The
 CC present nucleic acid sequence is that of the human Rhbg gene located on
 CC chromosome 1q21.3. This sequence encodes the human Rhbg protein of the
 CC invention. Rhbg is a polypeptide transporter-type protein.
 XX
 SQ Sequence 1805 BP; 351 A; 550 C; 515 G; 389 T; 0 other;
 Query Match 14.1%; Score 177; DB 24; Length 1805;
 Best Local Similarity 49.5%; Pred. NO. 1.1e-40;
 Matches 456; Conservative 0; Mismatches 465; Indels 0; Gaps 0;
 QY 141 CTATCAAGTTGGCCAGATGTCGACCTGATGGCGCCATGGCTTGGGCTTCCTCACTC 200
 DB 218 CTACCAAGCTTCAGAGACCTGATGCTGCTTGTGGCTTGGCTTCCTCACTGCT 277
 QY 201 GAGTTCCGAGACACAGCTGAGAGCTGTCCTTCACCTTCATGCTGGCGCTTGG 260
 DB 278 CTTCCTGACAGCTTACGCTTACAGACGCTGGGCTTCACTTCTGCGCGCTTGGC 337
 QY 261 TGTGCAATGGGCAATCCTGCTGAGCGGCTTCTGAGCAGTTCCTTCTGGGAAGGCT 320
 DB 338 CTGCAAGTGTCCACATGCTGCTGCGGCTTCTCACTTCTCCAGCGTGGCCATCCA 397
 QY 321 CATCACTGTTCAATGCTGCGCTGCGCACCATGATGCTTGTGCGTGCATGCTCACT 380
 DB 398 TGTGGGGTGGAGACATGATGATGCTGCTTGTGCGGGGCGCTGCTCACTCTT 457
 QY 381 GGATGCTGTTGGGGAAGGCTCACTGGCGCAGTGGTGCTGATGCTGCTGAGAGT 440
 DB 458 TGTGCGCTGCTGGGCAAGACCGGGCTTACCACTGCTGCTGCTGCGCTGAGAGT 517
 QY 441 GACAGCTTTAGGCAAGCTGAGGATGCTCACTCACTCACTCACTCACTCACTCACT 500
 DB 518 GGTGCTGTTGGCAATGATGATGCTTCTTCACTTCTGCGGGGTGAGAGATGCGCG 577
 QY 501 GACATGATGACATCTACGCTGTCGAGCCTATTTGGGCTGCTGCTGCGCTGCTGCT 560
 DB 578 AGGCTCATGATGATGACACCTTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 637
 QY 561 GCCAAGCCTCTACCCGAGGAGACGAGGATTAAGATCAGACAGCAACGATACCACTT 620

DB 638 GTACAGGCCCCAGCTGAGAGAGACCAAGACCCAGGCGCTCGCTACATTCAGACT 697
 QY 621 GTCTGCCATGCTGGGCGCCCTCTCTTGTGATGTTGTGGCAAGTTCAACTGTGCT 680
 DB 698 CTTCGCCATGATTTGGGACCATCTTCTGCTGATCTTGTGGCTTCACTCACTGCTGACT 757
 QY 681 GCTGAGAAATCCATTCGAAAGAAATGCGCTGTTCAACACCTACTATGCTGAGACT 740
 DB 758 CACAGCGCTGGGGCTGGGACGATCGAGCGGCCCTCAACACATACTACTCCCTGGCTGC 817
 QY 741 CAGCGTGTGACACCATCTCAGGCTATCTTGGCTCACCCCCAAGGAAGATCAGCA 800
 DB 818 CAGCACCCCTGGGCACTTGTGCTTGTGAGGAGAGATGAGATGAGAGCTTGCAT 877
 QY 801 GACTTATGTGACAGCTGCGGCTGTTGGAGAGGCGGTGGCTGCTGCTGCTGCTGCT 860
 DB 878 GGTCCACATCCAAATATGACGCTGCTGGAGGGGCTTGTGGGACCTCACTGAAAT 937
 QY 861 GATCCCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920
 DB 938 GATGCTGACACCCCTTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 997
 QY 921 GGAAGCAAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 980
 DB 998 GGGGTACAAAGTTCTTACGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1057
 QY 981 CATGGGTACAACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1040
 DB 1058 AGTCCACAACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1117
 QY 1041 GGTCTGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1061
 DB 1118 TGGACTTGGCACCATGAGC 1138
 RESULT 3
 AB211480
 ID AB211480 standard; cDNA; 1792 BP.
 XX
 AC AB211480;
 XX
 DT 20-JAN-2003 (first entry)
 XX
 DE Human polynucleotide seq ID NO 362.
 XX
 KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KW arthritis; cytostatic; immunomodulator; neoplastic; neuroprotective;
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 KW haemostatic; vunerary; fungicide; antibacterial; virucide; protozoacide;
 KW antilethritic; gene; ss.
 KW
 OS Homo sapiens.
 XX
 OS
 PN WO200270539-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 05-MAR-2002; 2002WO-US05095.
 XX
 PR 05-MAR-2001; 2001US-0799451.
 XX
 PA (HYSE-) HYSE INC.
 XX
 PI Tang YF, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac R;
 DR WPI: 2002-759812/82.
 DR P-PSDB; ABP69263.
 XX

Db 441 TGGGGCAGTCTGGGTAAGTCAGCCCATTCAGTGCATCATGACTTCTTCCAGT 500
 QY 441 GACAGCTTAGGCAACCGAGAGATGTCATCATATATCTTCAACACAGATATTACACAT 500
 Db 501 GACCCCTTTCGCTGTAATGAGTTTCTTCTTAACCTGGTAAAGATGACAG 560
 QY 501 GAACATGATGACATCTAGTGTGTGACAGCCATATTTGGGCTGTGTGGCTGTGCT 560
 Db 561 AGGCTCCATGACATCCACACATTTGGGCTTGTGGCTTCAAGATGACCCGATCCT 620
 QY 561 GCCAAAGCTCTACCCGAGGAGACGAGATTAAGATGACAGACGATACCCAGTTT 620
 Db 621 CTACGACGCAACCTAGACAGAGAGAGAGACAGAAATCTGTACCAAGTCGACCT 680
 QY 621 GTCGCAATGTCGGGCGCCCTTCTTGTGATGTTCGAGCCCAAGTTTCACTGTCTCT 680
 Db 681 CTTCGCAATGATGGACCCCTTCTTGTGATGTTCGAGCCCAAGTTTCACTGTCTCT 740
 QY 681 GCTGAGAGTCCAAATCGAAAGAGATGTCGCTTCAACACCTATGCTGTAGCAGT 740
 Db 741 ATCTACATGAGGAGACAGACAGACAGCCGACCACTCAACACTTGTCTGTGACG 800
 QY 741 CAGCTGTGACAGGCAATCTCAGGGTCAATCTTGGCTCAACCCCAAGGAGATGACGAA 800
 Db 801 CTGCTGCTTACCTCGTGGGCAATATCCAGTCCCTGCACAGAAAGGCAAGCTGACAT 860
 QY 801 GACTATGTGACACATGCGGCTGTGGCAGAGAGCCTGGCTGTGGTACTCTGTACCT 860
 Db 861 GGTGACATTCAGAAATGCGACCCCTGCGAGAGAGGGGTGGGCTGCGTCAAGAT 920
 QY 861 GATCCCTTCTCGGTGGTGGTCCATGTGCTGAGTGTGGGCTGATCTCGTCTG 920
 Db 921 GATGCTCATGCTTACGGTGGCTTCATCATGCGCTTCTGCTGCGCATCATCCACT 980
 QY 921 GGGAGCCAGTACCTGCGGGGTGTGTAAACCAAGTCTGGGATCCCAACAGCTCAT 980
 Db 981 GGGTTTGTATACCTGACCCCAATTCCTGAGTCCCGGCGACATCCAGAGACATGTGG 1040
 QY 981 CATGGGTCACAACTCAGCTTGTGGGTCTGCTTGGAGAGATCATCTATGTG 1055
 Db 1041 CATTAACAATTCGATGCGATTCGTGCAATACAGGCGGATCGTGGTGTG 1095

RESULT 7
 ABX76257 standard; DNA; 1968 BP.

XX AC ABX76257;
 XX
 DE 02-APR-2003 (first entry)
 XX
 XX Lung cancer-associated polynucleotide #123.
 XX
 KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
 KW antiinflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 OS Unidentified.
 PN WO200286443-A2.
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US12476.
 PR 18-APR-2001; 2001US-284770P.
 PR 10-MAY-2001; 2001US-290492P.
 PR 09-NOV-2001; 2001US-339245P.
 PR 13-NOV-2001; 2001US-350666P.
 PR 29-NOV-2001; 2001US-334370P.

PR 12-APR-2002; 2002US-372246P.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX Aziz N, Murray R;
 DR WPI: 2003-093161/08.
 DR P-PSDB; ABUS6530.
 PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 expression in lung cancer
 PS Claim 22; Page 285-286; 453pp; English.

CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung
 CC cancer-associated polynucleotides and polypeptides are used for
 CC identifying a compound that modulates a lung cancer-associated
 CC polypeptide, for inhibiting proliferation of a lung cancer-associated
 CC cell to treat lung cancer in a patient and for treating a mammal having
 CC lung cancer by administering a modulatory compound identified. The
 CC methods are useful for treating lung cancer, such as small cell lung
 CC cancer, non-small cell lung cancer or other benign or precancerous
 CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
 CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
 CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
 CC and polypeptides are useful for diagnostic purposes and as targets for
 CC screening for therapeutic compounds that modulate lung cancer, such as
 CC antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated
 CC polynucleotides of the invention.

SQ Sequence 1968 BP; 400 A; 592 C; 529 G; 445 T; 2 other;

Query Match 13.2%; Score 165.4; DB 25; Length 1968;
 Best Local Similarity 49.1%; Pred. No. 2.8e-37;
 Matches 439; Conservative 0; Mismatches 456; Indels 0; Gaps 0;

QY 141 CTATCAAGTTGGCAAGATCTGACGTCGATGAGGCGCATTTGGGCTTCTCTACCTC 200
 Db 217 CTACCCAGCTTCCAGAGAGTGCAGCTGATGCTTGTGGGCTTCTCTCATATGAC 276
 QY 201 GAGTTCCGAGACACAGCTGAGCAGTGTGCTTCAACCTTCTATGCTGGCGCTTGG 260
 Db 277 TTTCTGACAGCGCTTACGGCTTTCAGCGCGTGGCTTCAACTTCTGTGGACCTTTCG 336
 QY 261 TGTGCAAGTGGCAATCTGCTGACGCTTCTCGACCGAGTTCCTTGGGAAGTGTGT 320
 Db 337 CATCCAGTGGGCGCTCTCATGACGAGGCTGGTTCACCTTCAAGACCGCTACATTCGT 396
 QY 321 CATCAACAGTTTCAAGATTCGCTGCGCCACCATGAGTGTGCTGTGATCTCAGT 380
 Db 397 CGTGGGCGTGGAGAACCTTATCAAGCTGACTTCTGCGGCTCTGTCTGTGGCTT 456
 QY 381 GGAATGCTGTCTGGGAGAGTCAACTTGGGCGAGTTGTGTGATGCTGTGTGAGGT 440
 Db 457 TGGGGCAGTTCTGGGTAAGTAGGCCCATTCAGTGTCTATCATGACTTCTTCCAAAGT 516
 QY 441 GACAGCTTAAAGCAACCTGAGATGCTCATCATATATCTTCAACAGACTTACACAT 500
 Db 517 GACCCCTTTCGCTGTAATGAGTTCTTCTTAACCTGTAAGAGTGAAGATGACAG 576
 QY 501 GAACATGATGACATCTAGCTGTGTCAGACCTTATTTTGGGCTGTGTGGCTGTGCT 560
 Db 577 AGGCTCATATGACATTCACACATTTTGGGCTTCTTGTGGCTTACAGTACCCGATCCT 636
 QY 561 GCCAAAGCTCTACCCGAGGAGACGAGATTAAGATGACAGACGATACCCAGTTT 620
 Db 637 CTACGACGCAACCTAGACGAGAGCAAGAGAGACAGAAATTTCTGTACAGTGGACCT 696

OY		621	GTCGCAATGCCTGGGGCCGCTTCTGTGTGAATGTTTGCGCCAATTCCACTCTGCTCT	680
Dd		697	CTTTGGCATTGATGGCACCTCTCTCTGTGAATGATGAGGCCACCTTCAACTCGGCAT	756
OY		681	GCTGAGAAGTCCAAATCGAAGAGAAATAGCCGTGTTCACAACCTACTTGTGTAGCAAT	740
Dd		757	ATCTCAACATGGGGACACCCAGCACCCGACCCTCAACACTTCTGCTCTTGGCAGC	816
OY		741	CAGCGTGGTGACAGCCATCTCAGGGTCTCTTGGCTACCCCCCAAGGAAGATCAGCAA	800
Dd		817	CTGGGTGCTTAACCTCGGTGGCAATAATTCAGTAGCCCTTGCAACAAGAGGGCAAGCTGGACAT	876
OY		801	GACTTATGTGCACAGTGGGGTGTGTGGCAGAGAGCGTGGCTGTGGTACTGTGTACCT	860
Dd		877	GGTCACATCCAGATGGACAGCTCGCAGGAGGGGTGGCCGTGGGTACCGTGTGTGAAT	936
OY		861	GATCCCTTCTCCGAGGCTTGGCATGATGATCGTGGGCTTGTGGCTGGGGCTGATCTCCGTGGG	920
Dd		937	GATGCTCATGCTTTACAGSTGCTCCCTCATCATATGCGCTTCTGTGCGCATCATCTCCACCT	996
OY		921	GGGAGCCAAATACCTGCCCAGGGGTGTGTAAACGAAATGCTGGGGATTTCCCAACAGCTTCAT	980
Dd		997	GGGTTTGTATACCTGAGCCCATCTTCCTGTGAGATCCCGGCTGCACATCCAGAACATATGGG	1056
OY		981	CATGGGCTACAACTTCACTTCTGCTGGTCTGTGTGGAGATCATCTTCATTTGTG	1035
Dd		1057	CATTAAACAATGTGATGGCATTTCTCGGATCATATAGGCGCGCATCTGGGGTGGCTGTG	1111

[illegible]

Db 759 ATCTACATGGGGAGACAGCAGCAGCCGCGCATCAACACCTACTGCTCTTGGCAGC 818
QY 741 CAGCGTGGTACAGCCATCTCAGGCTATCTTGGCTGACCCCAAGGAGATCAGCAA 800
Db 819 CTGGTGTCTTACCTCCGCTGGCAATATCAGTGCCTTCACAGAAAGGCAAGCTGGACAT 878
QY 801 GACTTATGTGCACAGTGGCGGTGTGGCAGAGAGGCGTGGCTGTGATCTGTCACCT 860
Db 879 GGTGCACATCCAGATGACAGCTCGCAGAGAGGCGTGGCTGTGATCTGTCACAT 938
QY 861 GATCCCTTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 920
Db 939 GATGCTCATGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 998
QY 921 GGGAGCCAGTACCTGGCGGGGTGTGTAAACCGAGTGGGAGTCCCCACAGCTCAT 980
Db 999 GGGTTTGTATACCTGACCCCATCTCCGAGTCCCGGCTGCACATCCAGGACACATGTGG 1058
QY 981 CATGGCTACAACTTACAGCTTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1035
Db 1059 CATTAACAATCTGATGGCATCTCTGGCATATAGCGCGCATCTGGGTGCTGTG 1113

RESULT 9

ABK12334 standard; cDNA; 1679 BP.

ABK12334;

05-JUN-2002 (first entry)

cDNA encoding mouse nonerythroid Rh glycoprotein Rhbg.

Mouse; nonerythroid Rh glycoprotein; Rhbg; Rhb; antibody; immunogen;

Rh type B transporter gene; polytypic transporter-type protein;

Ion transporter; chromosome 3; gene; ss.

Mus sp.

Mus sp.

polyA_signal

/tag= a
/product= "Mouse Rhbg protein"
1634..1639
/tag= b
/standard_name= "PolyA signal"
/note= "Atypical polyadenylation site"

W0200216396-A2.

28-FEB-2002.

17-AUG-2001; 2001WO-US25881.

21-AUG-2000; 2000US-226767P.

(NYBL-) NEW YORK BLOOD CENT INC.

Huang C, Liu Z;

WPI; 2002-280905/32.

P-PSDB; AAU78092.

Homologues of mouse or human nonerythroid Rh glycoproteins, Rhbg or RhbG,

respectively, useful in the production of antibodies which are useful

for detecting Rhbg or RhbG glycoproteins in a sample -

Claim 1; Fig 1a; 59pp; English.

The present invention relates to a new protein or peptide comprising an

amino acid sequence having at least 60% identity to a sequence comprising

455 (mouse nonerythroid Rh glycoprotein homologue (Rhbg)) or 458 (human

CC nonerythroid Rh glycoprotein homologue (Rhbg) amino acids, fully defined
CC in the specification. The antibody of the invention is useful for
CC detecting an Rhbg or an RhbG glycoprotein in a sample, by contacting the
CC sample with antibody under conditions suitable for binding, assessing the
CC specific binding to the antibody, and thus detecting the presence of an
CC epitope of Rhbg or RhbG in the sample. The nucleic acids of the invention
CC are useful as probes for detecting transporter genes and particularly Rh
CC type B transporter genes including e.g. NH₄⁺ ion transporters. The
CC present nucleic acid sequence is that of the mouse Rhbg gene located on
CC chromosome 3. This sequence encodes the mouse Rhbg protein of the
CC invention. Rhbg is a polytypic transporter-type protein.

SQ Sequence 1679 BP; 324 A; 491 C; 469 G; 395 T; 0 other;

Query Match 12.7%; Score 159.4; DB 24; Length 1679;

Best Local Similarity 48.3%; Pred. No. 1.4e-35;

Matches 445; Conservative 0; Mismatches 476; Indels 0; Gaps 0;

QY 141 CTATCAAGTTGGCCAGATCTGACCGTATGCGGCGCATTTGGCTTCCATCCATC 200
Db 209 CTACCAAGCTTCCAGATGTGACAGTATGCTATGCTTGGCTTGGCTTCCATGAT 268
QY 201 GAGTTCCGAGACACAGCTGAGCAGTGTGCTTCACTCTTCAATGCTGGCTTGG 260
Db 269 CTTCCTACAGCGGTACGCGCTTACGAGCAGTGTGCTTCACTCTTCCCTGCGCAGCTCAC 328
QY 261 TGTGAGTGGGCAATCTGCGAGCGCTTCCAGGCGCAGTTCCTTGGGAGAGTGTGT 320
Db 329 CCTGAGTGGGCGACACTGCTCCAGAGCTTCTCCATCTTCCACAGGCTGGCCATCCA 388
QY 321 CATCACTGTTCAATGATTCGCTGAGCAGCATGATGCTTGGCTGCTGATCTCACT 380
Db 389 TGTGGCGGTGAGAGTTGATCAACAGCTGATCTTGGCGGAGGTGTGATCTCTTT 448
QY 381 GATGCTCTTCTGGGAGAGCTCACTTGGCGCAGTGTGTGATGCTGCTGGAGAGT 440
Db 449 CGGGCTGCTTCTGGGAGAGCTGAGCGCCAGCTGCTGCTAAAGGCTCACTGAGGC 508
QY 441 GACAGCTTATGAGCACTGAGAGTGTATGATGATGATGATGATGATGATGATGAT 500
Db 509 AGTGTGTTTATGCTCAACAGATTTATCTACTAGTCTCTGGGGGTGAGAGATGCTGG 568
QY 501 GAACATGATGACATCTATGTTGCGACGCTATTTGGCTGTCTGCTGCTGCTGCT 560
Db 569 AGGTTCATGACATTTACACATTTTGGGCGCTACTTGGGCTGCTCTCTCAAGGCTCT 628
QY 561 GCCAAGGCTTACCCGAGGGAAGGAGATTAAGATGATGATGATGATGATGATGAT 620
Db 629 CTACAGATCCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 688
QY 621 GTCGCTGATGCTGGGCGGCTCTTCTGATGATGATGATGATGATGATGATGATGAT 680
Db 689 CTTCGCTGATGCTGGGCGGCTCTTCTGATGATGATGATGATGATGATGATGATGAT 748
QY 681 GCTGAGAGTCAATCGAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 740
Db 749 GACAGCGCTGGGAGATGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 808
QY 741 CAGCGTGTGACAGCATCTCAGGTCTATCTTGGCTCAACCCCAAGGAGATGACGAA 800
Db 809 AAGCACCCTCAGTACTTTCGCTTGTGACCCCTTGTACGTGAGTGAAGTGAAGTGA 868
QY 801 GACTTATGTGACAGTATGCTGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 860
Db 869 GGTCCAGCTCCAGAT 928
QY 861 GATCCCTTCTCCGCTTGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 920
Db 929 GATGCTGACACCTTGGGCGGCTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 988
QY 921 GGGAGCCAGATCTGCGGCGGTGTGTAACGAGATGCTGGGAGATTTCCCAAGCTCAT 980
Db 989 GGGGTATATAGTCTTACGCGCTATCTGAAATCAGATTTAAACGCAAGACACATGTGG 1048

CC Rhcg or and Rhcg glycoprotein in a sample. The present sequence
 CC represents the cDNA encoding the mouse Rhcg Rh type C glycoprotein
 CC (Rhcg) protein sequence of the invention. The gene encoding this
 CC protein is located on murine chromosome 7.

XX Sequence 2098 BP; 458 A; 594 C; 559 G; 487 T; 0 other;

Query Match 12.0%; Score 150.2; DB 24; Length 2098;
 Best Local Similarity 47.5%; Pred. No. 7.7e-33;
 Matches 446; Conservative 0; Mismatches 493; Indels 0; Gaps 0;

```

QY 97 CACTATGACGCTTCTTAGAGATCAAAAGGGCTCGGACATCCATCAAGTTGGCCAA 156
DB 258 CGCAGAACATCTCCAGGACCTGGAAGAGATTCTACTATCGCTACCCGACGCTCCAG 317
QY 157 GATCTGACCGTATATGCGGCGCATTTGGCTTGGCTTCTTCACTCCAGTTCCGGAGACAC 216
DB 318 GATGTACAGCGCATGCTCTTCTGCGGCTTGGCTTCTTCACTCCAGTTCCGGAGCGCTAC 377
QY 217 AGCTGAGCAGTGTGGCTTCAACCTTCTCATGCTGGGCGCTGTGTGAGTGGGCAATC 276
DB 378 GGGCTCAGGCGCTGTAGGCTTCAACTTCCGCTGGAGAGCTTGGGACATCCAGTGGCAGAC 437
QY 277 CTGCTGAGCGCTTCTTGAAGCAGTTCCTTCTGGAGAGTGTATCATCACACTGTTCACT 336
DB 438 CTCATGACAGGAGTGTCCATTACTTGAAGAAGCCACATTTGCTCCTGAGCGTCGAGAAC 497
QY 337 ATTGGGCTGGCCACCATAGTGTCTTGTGCGGTGATCTCATGTGATGATCTCTTGGGG 396
DB 488 ATCATCCAGCTGACGCTTCTGTGTGACATCTTCTGTGTGCGCTTGGGCGCTTCTTCAAGC 557
QY 397 AAGTCAACTTGGGCGAGTGTGTGTGATGATGCTGTGTGAGAGTGCACACTTAAAGCAAC 456
DB 558 AAGGTCAAGCGCATGACAGCTGCTCATTAAGACCTTCTTCAAGTGAATCTCTTACAGATG 617
QY 457 CTGAGAGTGTATCATGTAATATCTTCAACACAGACTACACATGAACTGATGATCATC 516
DB 618 AATGATTCATCTCTCTGAACTGATAGAGCAAAAGATGCAAGGGGCTCTATAGACATC 677
QY 517 TACGTTTCGCGCTATTTTGGGCTGTGTGTGCGCTGTGTGCTGCAAAAGCTCTACCC 576
DB 678 CACACATTTGGCGCTTACTTGTGCTCAACAGTGTGCTTCAACGAAAAAACCTG 737
QY 577 GAGGAGACGAGATTAAGATCAGACAGCAACGATACCCAGTTTGTCTCCATCTGGGC 636
DB 738 GATCAGAGCAACAGACAGACAGCTCAGTACACTCGGACCTTTTCCCATGATGGC 797
QY 637 GCCCTCTCTTGTGATGTTTGGCCAACTGCTGTCTGTGAGAAAGTCCAAATC 696
DB 798 ACCCTCTCTTGTGATGTTTGGCCAACTGCTGTCTGTGAGAAAGTCCAAATC 857
QY 697 GAAAGGAAGATCCCGTGTTCACACACTATGCTGTGACATGACGCTGGTGGACGCC 756
DB 858 GCCCAGACCGAGCAGCCCTCAATCACTCTCTTGTGGACGCGTGTGTAAACACA 917
QY 757 ATCTCAGGCTCATCTTGTGCTCACCCTCAAGGAAGATCAGAGAAGCTTATGTGACAGT 816
DB 918 GTGACAGTATCCAGTATGTATACAAAGAGGCAAGTGTGATGTGACATCCAGAT 977
QY 817 GCGGTGTGGCAGAGAGCGTGTGCTGTGACCTGTGATCCTGATCCCTTCTCCGTGG 876
DB 978 GCCAGCGTTGAGAGTGGGCTGTGGGACAGCTGCGGAGATGATGCTCACACCTTAC 1037
QY 877 CTTCGATGCTGCTGGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 936
DB 1038 GGGCGCTCTCATCTGTGGGCTTCTTGTGGGCAATTTCTCCACCTTAAAGTTGCATCTTA 1097
QY 937 CCGGGGTGTGTACAGAGTGTGTGGGATTTCCCAACAGCTCATCATGGGCTTACAATTC 996
DB 1098 AGCGCATTCCTGGAGTCCCGCTTGGCATCCAGAGACATGTGGCATTTACACAACGTCAC 1157
QY 997 AGCTTGTGGTGTGCTGTGGAGATCATCTACATTTG 1035

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DB 1158 GGCATTCCHGCATCATAGCGCGCATTTGTGGTGTG 1196

RESULT 12

ABA42886/C

ABA42886 standard; DNA; 486 BP.

ABA42886; (first entry)

Human breast cell single exon nucleic acid probe #1581.

Human: microarray; single exon probe; gene expression; breast;

disease; cancer; ss.

Homo sapiens.

WO200157271-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US00662.

04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632266.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR.

WPI; 2001-496933/54.

New spatially-addressable set of single exon nucleic acid probes,

useful for measuring gene expression in sample derived from human

breast, comprises number of single exon nucleic acid probes

Claim 1; SEQ ID NO 1581; 327bp + sequence listing; English.

The invention relates to a spatially-addressable set of single exon

nucleic acid probes for measuring gene expression in a sample derived

from human breast and Bt 474 cells. The method involves contacting

the probes with a collection of detectably labelled nucleic acids

derived from mRNA of human breast, and then measuring the label

bound to each probe of the microarray. The probes are useful for

verifying the expression of regions of genomic DNA predicted to

encode proteins. They are useful for gene discovery, and for

determining predisposition and/or prognosing breast disease. Gene

expression analysis is useful for assessing the toxicity of chemical

agents on cells. The microarray of this invention presents a far greater

diversity of probes for measuring gene expression, with far less bias

than expressed sequence tag microarrays. The method is suitable for

rapid production of functional information from genomic sequence. The

present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the

printed specification, but was obtained in electronic format directly

from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 486 BP; 137 A; 112 C; 112 G; 125 T; 0 other;

Query Match 11.1%; Score 139.8; DB 22; Length 486;

Best Local Similarity 92.5%; Pred. No. 3.7e-30;

Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

477 TATCTTCACACAGATATACATGAAATGATGACATCTAGTTCGACGACCATTT 536

458 TTTATTCAGACAGACTACACATGAACTGAGGACTTCTAGTGTTCGACGCTATTT 399

QY 537 TGGGCTGTCTGTGCTGGCTGGCTGCCAAGCCTTACCCGAGGGAAGGAGATTAAGA 596
|||||
Db 398 TGGGCTGTGACTGTGCTGGCTGGCTGCCAAGCCTTACCCGAGGGAAGGAGATTAAGA 339
597 TCAGACAGCAAGCATACCCAGTTGTCTGCCATGCTGGG 635
Db 338 TCAGACAGCAAGCATACCCAGTTGTCTGCCATGCTGGG 300

RESULT 13

ABAS3307/c
ID ABAS3307 standard; DNA: 486 BP.

AC ABAS3307;

DT 01-FEB-2002 (first entry)

DE Human foetal liver single exon nucleic acid probe #1612.

DE Human: foetal liver: gene expression: single exon nucleic acid probe: ss.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00669.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

PT WPI; 2001-483447/52.

PS Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human fetal liver -

XX Claim 1; SEQ ID NO 1612; 639pp + sequence listing; English.

CC The invention relates to a single exon nucleic acid probe for

CC measuring human gene expression in a sample derived from human foetal

CC liver. The single exon nucleic acid probes may be used for predicting,

CC measuring and displaying gene expression in samples derived from human

CC fetal liver. The present sequence is a single exon nucleic acid

CC probe of the invention.

CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 486 BP; 137 A; 112 C; 112 G; 125 T; 0 other;

Query Match 11.1%; Score 139.8; DB 22; Length 486;
Best Local Similarity 92.5%; Pred. No. 3.7e-30;

Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 477 TATCTCAACAGCACTACACATCAATGAATGACACATCTAGCTGTGCGACCTATTT 536
|||||

Db 458 TTTATTGACAGACGACTACACATGAACCTGAGGCACTTCTACGCTTGGACCTATTT 399
|||||

QY 537 TGGGCTGTCTGTGCTGGCTGGCTGCCAAGCCTTACCCGAGGGAAGGAGATTAAGA 596
|||||

Db 398 TGGGCTGTGACTGTGCTGGCTGGCTGCCAAGCCTTACCCGAGGGAAGGAGATTAAGA 339
|||||

QY 597 TCAGACAGCAAGCATACCCAGTTGTCTGCCATGCTGGG 635
|||||

Db 338 TCAGACAGCAAGCATACCCAGTTGTCTGCCATGCTGGG 300
|||||

RESULT 14

ABA23081/c
ID ABA23081 standard; DNA: 486 BP.

AC ABA23081;

DT 23-JAN-2002 (first entry)

DE Probe #1547 for gene expression analysis in human heart cell sample.

DE Human: gene expression: heart; microarray; vascular system; probe;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease: ss.

OS Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00666.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

PT WPI; 2001-488899/53.

PS Single exon nucleic acid probes for analyzing gene expression in human

PT hearts -

XX Claim 1; SEQ ID NO 1547; 530pp; English.

CC The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart. The

CC present sequence is one such probe. The probes may be used for

CC predicting, measuring and displaying gene expression in samples derived

CC from the human heart via microarrays. By measuring gene expression, the

CC probes are useful for predicting, diagnosing, grading, staging,

CC monitoring and prognosing diseases of the human heart and vascular system

CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and

CC congenital heart disease.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 486 BP; 137 A; 112 C; 112 G; 125 T; 0 other;

Query Match 11.1%; Score 139.8; DB 22; Length 486;
Best Local Similarity 92.5%; Pred. No. 3.7e-30;

Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 477 TATCTCAACAGCACTACACATCAATGAATGACACATCTAGCTGTGCGACCTATTT 536
|||||

Db 458 TTTATTGACAGACGACTACACATGAACCTGAGGCACTTCTACGCTTGGACCTATTT 399
|||||

QY 537 TGGGCTGTCTGTGCTGGCTGGCTGCCAAGCCTTACCCGAGGGAAGGAGATTAAGA 596
|||||

Db 398 TGGGCTGTGACTGTGCTGGCTGGCTGCCAAGCCTTACCCGAGGGAAGGAGATTAAGA 339
|||||

QY 597 TCAGACAGCAAGCATACCCAGTTGTCTGCCATGCTGGG 635
|||||

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Db 91 GAAGCAGCTCTCATTCCTCTCTCTATTTTAAACCACATGACGCTTCTTAGAGAT 150
QY 121 CAAAGGGGCTGCTGGCATCTATCAAGTTGGCCAGATCTGACCGTGATGGGCCATT 180
Db 151 CAAAGGGGCTGCTGGCATCTATCAAGTTGGCCAGATCTGACCGTGATGGGCCATT 210
QY 181 GGGTGGGCTCTCTACCTGAGTTTCCGAGACACAGCTGGAGCACTGTGGCTTCAAC 240
Db 211 GGGTGGGCTCTCTACCTGAGTTTCCGAGACACAGCTGGAGCACTGTGGCTTCAAC 270
QY 241 CTCTCATGCTGGCGCTTGGTGACATGGGCAATCTGCTGGACGCTTCTGAGCAG 300
Db 271 CTCTCATGCTGGCGCTTGGTGACATGGGCAATCTGCTGGACGCTTCTGAGCAG 330
QY 301 TTCCCTTCTGGAGAGTGATCACACTGTTCAATTCGCTGGCGCACCATTAGTGTCT 360
Db 331 TTCCCTTCTGGAGAGTGATCACACTGTTCAATTCGCTGGCGCACCATTAGTGTCT 390
QY 361 TTGTCGGTGTGATCTCAGTGATGCTGTTGGGGAAGTCAACTTGGCGCAGTTGGTG 420
Db 391 ATGTCGGTGTGATCTCAGTGATGCTGTTGGGGAAGTCAACTTGGCGCAGTTGGTG 450
QY 421 GTGATGGTGTGGAGAGTGACAGCTTTAGGCACTGAGGATGGTCACTAGTAATATC 480
Db 451 GTGATGGTGTGGAGAGTGACAGCTTTAGGCACTGAGGATGGTCACTAGTAATATC 510
QY 481 TTCAACACAGACTACACATGAACTGATGACATCTACGTGTTCGAGCCTATTTTGGG 540
Db 511 TTCAACACAGACTACACATGAACTGATGACATCTACGTGTTCGAGCCTATTTTGGG 570
QY 541 CTGTCGTGGCTGGTGCTGGTCCAAAGCCTTACCCGAGGGAACGAGATTAAGATCAG 600
Db 571 CTGTCGTGGCTGGTGCTGGTCCAAAGCCTTACCCGAGGGAACGAGATTAAGATCAG 630
QY 601 ACAGCAGCATACCCAGTTTGTCTGCATGCTGGGCGCCTTCTTGTGATGTTCTG 660
Db 631 AGAGCAAGCATACCCAGTTTGTCTGCATGCTGGGCGCCTTCTTGTGATGTTCTG 690
QY 661 CCAAGTTTCACTGCTGCTGCTGAGAGTCCAAATGGAAGAAATGCGGTTCAC 720
Db 691 CCAAGTTTCACTGCTGCTGCTGAGAGTCCAAATGGAAGAAATGCGGTTCAC 750
QY 721 ACCTACTATGCTAGACAGTCAAGTGGTGAACCATCTCAGGGTCACTTGGCTCAC 780
Db 751 ACCTACTATGCTAGACAGTCAAGTGGTGAACCATCTCAGGGTCACTTGGCTCAC 810
QY 781 CCCCAGGGAAGATCAGCAAGACTTAATGTCACAGTGGGCTGTGGCAGAGGCGTGGCT 840
Db 811 CCCCAGGGAAGATCAGCAAGACTTAATGTCACAGTGGGCTGTGGCAGAGGCGTGGCT 870
QY 841 GTGGGTACCTGCTGACCTGATCCCTTCCGTGGCTTGCATGCTGCTGCTTGTG 900
Db 871 GTGGGTACCTGCTGACCTGATCCCTTCCGTGGCTTGCATGCTGCTGCTTGTG 930
QY 901 GCTGGGCTGATCTCCGTCGGGGGAGCCAGTACCTGCCGGGTGTGTAACGAGTGTG 960
Db 931 GCTGGGCTGATCTCCGTCGGGGGAGCCAGTACCTGCCGGGTGTGTAACGAGTGTG 990
QY 961 GGGATTCACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Db 991 GGGATTCACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1050
QY 1021 ATCATCTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1051 ATCATCTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1110
QY 1081 TTCCAGGCTCTCTCAGCATTTGGGGAATCAGCTTGGCCATCTGATAGCTCAGCTCT 1140
Db 1111 TTCCAGGCTCTCTCAGCATTTGGGGAATCAGCTTGGCCATCTGATAGCTCAGCTCT 1170
QY 1141 GGTCTCTGACAGGTTGGTCTCTAAATCTTAAATATGGAAGACACCTCATGAGGCTTAA 1200
Db 1171 GGTCTCTGACAGGTTGGTCTCTAAATCTTAAATATGGAAGACACCTCATGAGGCTTAA 1230

QY 1201 TATTTGATGACCAAGTTTCTGGAAGTTTCTCATATTGGCTGTGATTTTAA 1254
Db 1231 TATTTGATGACCAAGTTTCTGGAAGTTTCTCATATTGGCTGTGATTTTAA 1284
RESULT 2
US-08-553-888A-2
Sequence 2, Application US/08553888A
Patent No. 5723293
GENERAL INFORMATION:
APPLICANT: Huang
TITLE OF INVENTION: DIAGNOSTIC METHOD AND KIT FOR
NUMBER OF INVENTION: DETERMINING RH BLOOD GROUP GENOTYPE
CORRESPONDENCE ADDRESSES: 3
ADDRESSEE: Hoffmann & Baron, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: USA
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553, 888A
FILING DATE: 11/06/95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: O'Dea, Sean W.
REGISTRATION NUMBER: 37690
REFERENCE/DOCKET NUMBER: 454-5
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1466 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-553-888A-2
Query Match 94.3%; Score 1182; DB 1; Length 1466;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1209; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 1 ATGAGCTTAAGTACCCGCGGCTGTGTCGCGCTGCTGCCCTCTGGGCCCTAAGACTG 60
Db 45 ATGAGCTTAAGTACCCGCGGCTGTGTCGCGCTGCTGCCCTCTGGGCCCTAAGACTG 104
QY 61 GAAGCAGCTCTCATTTCTCTCTCTCTATTTTAAACCACATGACGCTTCTTAGAGAT 120
Db 105 GAAGCAGCTCTCATTTCTCTCTCTCTATTTTAAACCACATGACGCTTCTTAGAGAT 164
QY 121 CAAAGGGGCTGCTGGCATCTATCAAGTTGGCCAGATCTGACCGTGATGGGCCATT 180
Db 165 CAAAGGGGCTGCTGGCATCTATCAAGTTGGCCAGATCTGACCGTGATGGGCCATT 224
QY 181 GGGTGGGCTCTCTACCTGAGTTTCCGAGACACAGCTGGAGCACTGTGGCTTCAAC 240
Db 225 GGGTGGGCTCTCTACCTGAGTTTCCGAGACACAGCTGGAGCACTGTGGCTTCAAC 284
QY 241 CTCTTATGCTGGCGCTTGGTGACATGGGCAATCTGCTGGACGCTTCTGAGCAG 300
Db 285 CTCTTATGCTGGCGCTTGGTGACATGGGCAATCTGCTGGACGCTTCTGAGCAG 344
QY 301 TTCCCTTCTGGAGAGTGATCACACTGTTCAATTCGCTGGCGCACCATTAGTGTCT 360
Db 345 TTCCCTTCTGGAGAGTGATCACACTGTTCAATTCGCTGGCGCACCATTAGTGTCT 404

QY	361	TTGCGCGTGGATCTCAGTGGAGTGCMTCTGGGGAAAGTCACTTGGCGCACTGGTGTG	420
Db	405	ATGTCGGTCTGATCTTACGCGGTGCTGTCTTGGGGAAAGTCACTTGGCGCACTGGTGTG	464
QY	421	GTGATGGTGGTGGTGGAGGTGACAGCTTATAGCAACTGAGGANGTGCATCATTAATATC	480
Db	465	GTGATGGTGGTGGTGGAGGTGACAGCTTATAGCAACTGAGGANGTGCATCATTAATATC	524
QY	481	TTCAACACAGACTACCAATGATGACATCTTACGTGTTCGACCTATTTTGGG	540
Db	525	TTCAACACAGACTACCAATGATGACATCTTACGTGTTCGACCTATTTTGGG	584
QY	541	CTGCTGTGGGCGTGTGGTGGCCAAAGCGCTTACCCGAGGGAAAGGAGATTAAGATCAG	600
Db	585	CTGACTGTGGCGTGTGGTGGCCAAAGCGCTTACCCGAGGGAAAGGAGATTAAGATCAG	644
QY	601	ACAGCAACGATATCCAGTTTGTCTGCGCATGCTGGGCGCCCTCTTCTGTGATGTTCGG	660
Db	645	AGAGCAACGATATCCAGTTTGTCTGCGCATGCTGGGCGCCCTCTTCTGTGATGTTCGG	704
QY	661	CCAAGTTTCAACTGTGCTGTGCTGAGAAAGTCCAATCCAAAGGAAGATGCCGTTCAC	720
Db	705	CCAAGTTTCAACTGTGCTGTGCTGAGAAAGTCCAATCCAAAGGAAGATGCCATGTTCAC	764
QY	721	ACCACATATGCTGTAGCAGTCAAGCGTGGTGCACACCAATCTCAGGGTCACTCTTGGCTAC	780
Db	765	ACCACATATGCTGTAGCAGTCAAGCGTGGTGCACACCAATCTCAGGGTCACTCTTGGCTAC	824
QY	781	CCCCAAGGGAAGATCAGCAAGACTTATGTGCACAGTGGCGGTGTGGCAGAGGCGTGCT	840
Db	825	CCCCAAGGGAAGATCAGCAAGACTTATGTGTGCACAGTGGCGGTGTGGCAGAGGCGTGCT	884
QY	841	GTGGGTACCTGCTTCACTGTATCCCTTCTCCGTGGCTTGGCATTGTGCTGGGCTTGTG	900
Db	885	GTGGGTACCTGCTTCACTGTATCCCTTCTCCGTGGCTTGGCATTGTGCTGGGCTTGTG	944
QY	901	GCTGGCGTGAATCTCCGTGCGGGGAGCAAGTACTGCCGCGGGGTGTGTAACCGAGTGTG	960
Db	945	GCTGGCGTGAATCTCCATGCGGGGAGCAAGTACTGCCGCGGGGTGTGTAACCGAGTGTG	1004
QY	961	GGGATTTCCCAACAGCTCCATCATGAGGCTTACAACTTCAGCTTGGTGGTCTCTTGGAGAG	1020
Db	1005	GGGATTTCCCAACAGCTCCATCATGAGGCTTACAACTTCAGCTTGGTGGTCTCTTGGAGAG	1064
QY	1021	ATCATTTACATTTGCTGCTGGTGTGATACCGTCGCGGAGCGCGGAATGAGATGATGGC	1084
Db	1065	ATCATTTACATTTGCTGCTGGTGTGATACCGTCGCGGAGCGCGGAATGAGATGATGGC	1124
QY	1081	TTCCAGGTCTCCTCAGCATTGGGGAACTCAGCTTGGGCATCTGATAGCTCCTCAGCTCT	1144
Db	1125	TTCCAGGTCTCCTCAGCATTGGGGAACTCAGCTTGGGCATCTGATAGCTCCTCAGCTCT	1188
QY	1141	GGTCTCTGACAGCTTGGTCTCTTAATCTTAAATATGGAAGCACTCATGAGGCTAAA	1200
Db	1185	GGTCTCTGACAGCTTGGTCTCTTAATCTTAAATATGGAAGCACTCATGAGGCTAAA	1244
QY	1201	TATTTTGTGACCAAGTTTCTGGAAGTTCTCATTTGGGTGTGGATTTTAA	1254
Db	1245	TATTTTGTGACCAAGTTTCTGGAAGTTCTCATTTGGGTGTGGATTTTAA	1298
RESULT 3			
US-09-461-325-75			
; Sequence 75, Application US/09461325A			
; Patent No. 6475753			
; GENERAL INFORMATION:			
; APPLICANT: Ruben et al.			
; TITLE OF INVENTION: 94 Human Secreted Proteins			
; FILE REFERENCE: P2029p1			
; CURRENT APPLICATION NUMBER: US/09/461,325A			
; CURRENT FILING DATE: 1999-12-14			
; EARLIER APPLICATION NUMBER: PCT/US99/13418			

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? EARLIER FILING DATE: 1999-06-15
? EARLIER APPLICATION NUMBER: 60/089,507
? EARLIER FILING DATE: 1998-06-16
? EARLIER APPLICATION NUMBER: 60/089,508
? EARLIER FILING DATE: 1998-06-16
? EARLIER APPLICATION NUMBER: 60/089,509
? EARLIER FILING DATE: 1998-06-16
? EARLIER APPLICATION NUMBER: 60/089,510
? EARLIER FILING DATE: 1998-06-16
? EARLIER APPLICATION NUMBER: 60/090,112
? EARLIER FILING DATE: 1998-06-22
? EARLIER APPLICATION NUMBER: 60/090,113
? EARLIER FILING DATE: 1998-06-22
? NUMBER OF SEO ID NOS: 532
? SOFTWARE: PatentIn Ver. 2.0
? SEO ID NO 75
? LENGTH: 1650
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-461-325-75

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Query Match	8.7%;	Score 109.6;	DB 4;	Length 1650;
Best Local Similarity	48.7%;	Pred. No. 4.5e-23;		
Matches 327;	Conservative 0;	Mismatches 344;	Indels 1;	Gaps 1;

QY	364	CCGGGCGTCACTCAGTGGATGCTGTCCTTGGGGAAAGGTCACATTGGCCAGTGGTGCTG	423
Db	33	TCGTGTCGCGTGCCCTTTGGGGCAGTCTGGGTAAAGTCAGCCCATTCACGCTGCTATC	92
QY	424	ATGTGCTGCTGGAGGTGACAGCTTTAGGCAACCGAGAGTGTGTCATCAGTAATATCTTC	483
Db	93	ATGACTTTCTTCCAGGTAGCCCTCTTCGCTGGAATGAGTTCATTCCTCTTAACCTGCTA	152
QY	484	AACACAGACTACACATATGATATGACATCTCTACGTTGCGACGCTTATTTGGGCTG	543
Db	153	AAGGTGAAGGATGACAGAGGCTCCATGACATCCACACATTTGGGCGCTACTTGGGCTC	212
QY	544	TCTGTGGCCTGGTGCCCTGCCAAAGCCTCTACCCGAGGGAGAGAGATAAAGATAGACA	603
Db	213	ACAGTGACCCGGATCTCTACCGACGCAACCTAGAGCAGAGACAGAGACAGAAATCT	272
QY	604	GCAACGATATCCAGTGTGTCTGCGCATGCTGGGGGCGCCCTCTTGTGGATGTTCTGGCCA	663
Db	273	GTTATCCAGTGGACCCCTTTGGCCATGGATGGCACCCCTTCTCTGTGATGATGTCAGGCC	332
QY	664	AGTTTCAACTCTGCTGCTGCTGAGAAAGTCCAAATCGAAAGAAAGATGCGGTGTTCAACAC	723
Db	333	AGCTTCAACTCAGCATATCTCATACATGGGAGACACCGACAGCAGCCGCGCATCAACAC	392
QY	724	TACTATGCTGTAGCAGTCAGCGTGGTGAACAGCCATCTCAGGGTCATCCTTGGCTCACCC	783
Db	393	TACTGCTCTTTGGCAGCCCTGGGTGGTCTTACCTCGGGCAAAATTC-CAGTGGCCCTCCAAAG	451
QY	784	CAAGGGAAGATACGACAAAGCTTATGTGACAGTGGGGTGTGGACGAGGCGCTGGCTG	843
Db	452	AAGGCAAGCTGACATGATGTCACATCCAGAATGCGACGCTGCGAGAGGGGTGGCCGTG	511
QY	844	GGTACCTGCTGACACTGATCCCTTCTCCGTGGCTTGGCAGTGGTCTGGGCTTGTGGCT	903
Db	512	GGTACCGCTGCTGAGATATGCTCATGCTTACGGTGGCCCTCATCATGAGGCTTCTCTGAC	571
QY	904	GGGCTGATCTCCGTGGGGGAGACCAAGTATCTGCGGGGTGTGTAACCGAGTGTGGGG	963
Db	572	GGCATCATCTCCACCCTGGGTTTGTATACCTGACGCCCATTCCTTGGAGTCCCGGCTGAC	631
QY	964	ATTCCCAACAGCTCCATGAGGGATACAACTTACACTTGGGGGTCTGCTTGGAGAGATC	1022
Db	632	ATCCAGACACATATGGGATTAACAATTCGATGTCATTCCTGGCATCATAGGCGGCATC	691
QY	1024	ATCTACATTG 1035	
Db	692	GTGGGTGCTG 703	

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6902
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6902

Query Match 3.2%; Score 40; DB 4; Length 801;
Best Local Similarity 47.9%; Pred. No. 0.04;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 236 TCACCTCTTCATGCTGGCCCTTGCTGTCAGTGGGCAATCCTGCTGGAGGCTTCTCTGA 295
DB 742 TCCTGCTCTGGGCGCCCTGCACTTCTGCTGCTGGCGGATCAAGAGCGCGCTTCATCA 683
QY 296 GCCAGTTCCCTTGGGAGGTGTCATCAGTGTTCAGTATTCGGCTGGCCACCATGA 355
DB 682 ACACCGTACACCGTGGCCAGGTGCTGCGGCTGTTCCGTTCATCTGATCTGCTGT 623
QY 356 GTGCTTTGCTGCTGCTGATCTCAGTGAGTCTGTTGGGGAAGTCACTTGGCGAGT 415
DB 622 TCCCTCTTCAAGCTGACATCTTCACCGCCGACATCTGGGGCAGACACCCGAGCTGG 563
QY 416 TGGTGGTATGCTGCTGGTGGAGGTGACACACTTTAGGCAACCTGAGAGTGTATCAGTA 475
DB 562 GCAGCGTATGAACCAAGTGTGCGCAACATGCTGTGCTACCGTGGTGTTCATCGGCA 503

RESULT 11
US-09-252-991A-6871/C
; Sequence 6871, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6871
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6871

Query Match 3.2%; Score 40; DB 4; Length 1410;
Best Local Similarity 47.9%; Pred. No. 0.056;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 236 TCACCTCTTCATGCTGGCGCTTGCTGTCAGTGGGCAATCCTGCTGGAGGCTTCTCTGA 295
DB 1046 TCCTGCTCTGGGCGCCCTGCACTTCTGCTGCTGGCGGATCAAGAGGCGCGCTTCATCA 987
QY 296 GCCAGTTCCCTTGGGAGGTGTCATCAGTGTTCAGTATTCGGCTGGCCACCATGA 355
DB 986 ACACCGTACACCGTGGCCAGGTGCTGCGGCTGTTCCGTTCATCTGATCTGCTGT 927

QY 356 GTGCTTTGCTGCTGCTGATCTCAGTGGATGCTGCTTGGGGAAGTCACTTGGCGAGT 415
DB 926 TCCCTTCAAGCTGACATCTTCACCGCCGACATCTGGGGCAGACCAACCCGAGCTGG 867
QY 416 TGGTGGTATGCTGCTGGTGGAGGTGACACCTTTAGGCAACCTGAGAGTGTATCAGTA 475
DB 866 GCAGCGTATGAACCAAGTGTGCGCAACATGATGCTGTGCTACCGTGGTGTTCATCGGCA 807

RESULT 12
US-09-252-991A-6850
; Sequence 6850, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6850
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6850

Query Match 3.2%; Score 40; DB 4; Length 1482;
Best Local Similarity 47.9%; Pred. No. 0.058;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 236 TCACCTCTTCATGCTGGCGCTTGCTGTCAGTGGGCAATCCTGCTGGAGGCTTCTCTGA 295
DB 417 TCCTGCTCTGGGCGCCCTGCACTTCTGCTGCTGGCGGATCAAGAGGCGCGCTTCATCA 476
QY 296 GCCAGTTCCCTTGGGAGGTGTCATCAGTGTTCAGTATTCGGCTGGCCACCATGA 355
DB 477 ACACCGTACACCGTGGCCAGGTGCTGCGGCTGTTCCGTTCATCTGATCTGCTGT 536
QY 356 GTGCTTTGCTGCTGCTGATCTCAGTGAGTCTGTTGGGGAAGTCACTTGGCGAGT 415
DB 537 TCCCTTCAAGCTGACATCTTCACCGCCGACATCTGGGGCAGACCAACCCGAGCTGG 596
QY 416 TGGTGGTATGCTGCTGGTGGAGGTGACACCTTTAGGCAACCTGAGAGTGTATCAGTA 475
DB 597 GCAGCGTATGAACCAAGTGTGCGCAACATGATGCTGTGCTACCGTGGTGTTCATCGGCA 656

RESULT 13
US-09-252-991A-6757
; Sequence 6757, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6757
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-6757

Query Match 3.2%; Score 40; DB 4; Length 1500;
Best Local Similarity 47.9%; Pred. No. 0.059;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 236 TCACCTTCATCTGCGCCCTGGTGGTGCAGTGGGCAATCGCTGAGCGGCTTCCTGA 295
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 455 TCGCTCTGGGCGCCCTGACATCTCTGCTGCTGGCGGAGCAAGAGGCGGCGCTTCATCA 514
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
QY 296 GCCAGTTCCTTCGGGAAGGTGTCATCACATCTGTCAGTATTCGGCTGGCCACCATGA 355
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 515 ACACCGTCACACCGCTGGCCAAAGGTCTGCGGCTGCTTCATCTGATCTGCTGT 574
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
QY 356 GTGCTTGTGCGTCTGATCTCATGTGATGCTGCTTGGGGAAGTCACATTCGGCGAGT 415
|| || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 575 TCGCTTCACAGCTGGACATCTTCACCGCCGACATCTGGGGCAAGACACCGGACCTGG 634
|| || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
QY 416 TGTGTGTATGTGCTGTGAGAGTGACAGCTTTCAGCAACCTGAGGATGCTCATAGTA 475
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 635 GCACGCTGATGACACAGGTGGCGCAACATGATGCTGTACCGCTGTGGGTGTTCACTGCA 694

RESULT 14

US-08-476-176B-15/C
; Sequence 15, Application US/08476176B
; Patent No. 5958708

GENERAL INFORMATION:

APPLICANT: Hardman, No. 5958708man
APPLICANT: Koldinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESS: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476.176B
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

NAME/KEY: CDS
LOCATION: 22..447
FEATURE:

NAME/KEY: mat_peptide
LOCATION: 79..447
OTHER INFORMATION: /product="heavy chain variable
OTHER INFORMATION: region C21-Hay1"
US-08-476-176B-15

Query Match 3.1%; Score 39.4; DB 2; Length 467;
Best Local Similarity 51.4%; Pred. No. 0.045;
Matches 91; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 264 GCAATGGCAATCTCTGTCGACGCGCTTCGACCACTTCCTTCTGGGAAGGTGTCAT 323
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Db 405 GTACCTGTAGTGTGCTGCGCGCTGAAGTGGCTGAACCTGGCGCAGTAGTACAGCGCGGTGC 346
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QY 324 CACACGTGTAGTATTCGGCGTGGCCACCATGATGTCCTTTCGGTGGTATCTCAGTGA 383
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 345 CTCCTGTCTCAGGCTGCTCAGCTCCATGATGAGCGGTGCTGCGCTGTGTGGCGGTGA 286
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
QY 384 TGTGTGTGGGGAAGTCACATTCGCGCACTGTGTGATGATGCTGTGTGAGGT 440
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Db 285 GTGGCGCTTGGCCTTGAACCTCTCGCTGTATGTTGTGTGATGAGGTGCGCGGCTGAT 229

RESULT 15

US-08-127-721A-15/C
; Sequence 15, Application US/08127721A
; Patent No. 6066718

GENERAL INFORMATION:

APPLICANT: Hardman, No. 6066718man
APPLICANT: Koldinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6066718artis Patent and Trademark Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127.721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6066718ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

NAME/KEY: CDS
LOCATION: 22..447
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 79..447

OTHER INFORMATION: /product= "heavy chain variable"
OTHER INFORMATION: region C21-Hay1
US-08-127-721A-15

Query Match 3.1%; Score 39.4; DB 3; Length 467;
Best Local Similarity 51.4%; Pred. No. 0.045;

Matches 91; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

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QY 264 GCAGTGGCAATCCTGCTGGACGCGCTTCCTGAGCCAGTTCCCTTGTGGAAGGTGTCAT 323
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 405 GTAGTGTGTAATGCTGCTGCGCTGAAGTGGCTGAACCTGCGCAGTAGTACAGGCGGTGTC 346
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 324 CACACTGTTCAGTATTCGGCTGGCCACCATGAGTCTTTGTGCGGTGCTGATCTCATGGA 383
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 345 CTCGCTGTGTCAGGCTGCTCAGCTCCATGTAGCGGCTGCTGCGCTGTGCGGCGGTGAA 286
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 384 TGCTGTCTTGGGGAAGGTCAACTTGGCGCAGTTGGTGATGATGATGCTGTGAGGT 440
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 285 GGTGGCCTTGCCCTTGAACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 229
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: September 26, 2003, 11:37:30
Job time : 96 secs

Db 176 GCAGAGAGCGCTGGCTTGGGTACCTGCTACCTATCCCTTCCGTGGCTTGCATG 235
QY 886 GTGCTGGGTCTGTGTGGCTGGCTGATCTCCGTCGGGGAGCCAAAGTACCTGCGGGGTGT 945
Db 236 GTGCTGGGTCTGTGTGGCTGGCTGATCTCCGTCGGGGAGCCAAAGTACCTGCGGGGTGT 295
QY 946 TGTAAACGAGTGTGGGGATTCGCCACAGCTCCATATGAGGCTACACTTCACTTGTGCTG 1005
Db 296 TGTAAACGAGTGTGGGGATTCGCCACAGCTCCATATGAGGCTACACTTCACTTGTGCTG 355
QY 1006 GGTCTGCTGGAGAGATCTACATATGTGTGCTGCTGTGATACCGTCGGAGCGCGG 1065
Db 356 GGTCTGCTGGAGAGATCTACATATGTGTGCTGCTGTGATACCGTCGGAGCGCGG 415
QY 1066 AATGGCATG 1074
Db 416 AATGGCATG 424

RESULT 2
US-09-949-145-5
; Sequence 5, Application US/0949145
; Patent No. US20020055622A1
; GENERAL INFORMATION:
; APPLICANT: New York Blood Center
; TITLE OF INVENTION: Mammalian No. US20020055622A1-erythroid Rh Type C Genes and Glyco
; FILE REFERENCE: Docket 454-31
; CURRENT APPLICATION NUMBER: US/09/949,145
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/230660
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-145-5

Query Match 13.2%; Score 165.4; DB 9; Length 1440;
Best Local Similarity 49.1%; Pred. No. 2.4e-42;
Matches 439; Conservative 0; Mismatches 456; Indels 0; Gaps 0;

QY 141 CTAATCAAGTTGGCCAAAGATCTGACCGTGTATGGCGGCCATTTGGCTTCCCTACCTC 200
Db 177 CTACCCAAAGCTTCCAGAGACGTGACGTGATGGTCTTCGTGGGCTTCGCTCTCATGAC 236
QY 201 GAGTTTCGGAGACAGCTGAGAGAGTGGGCTTCAACCTTCATCATCTGCGCTTGG 260
Db 237 TTTCCTGACGCGCTACGCGCTTCAAGCGCGTGGGCTTCAACCTTCTGTTGGACGCTTCGG 296
QY 261 TGTGAGTGGGCAATCTGCTGAGAGGCTTCTGAGCCAGTTCCTTCTGGGAAGGTGT 320
Db 297 CATCCAGTGGGCGGTGCTATGCAAGGCGTGGTTCACCTTCTTACAAGACCGCTACATCT 356
QY 321 CATCAACTGTTCAATATGCTGCTGCGCCACCATGATGCTGTTGCGGTGCTGATCTCACT 380
Db 357 CTGGGGCGTGGAGAACCTCATCAAGCTGACTTCTGCGGCTGTGCTGCGGGCTT 416
QY 381 GGATGCTGTCTGGGGAAGAGTCAACGTGGCGAGTTGGTGGATGGTCTGTTGAGAGT 440
Db 417 TGGGGCAGTTCTGGGTAAAGTACGCCCACTTCAAGCTGCTCATAGACTTCTTCCAAAT 476
QY 441 GACAGCTTTAGGCAACTGAGAGTGTATCACTAATATCTTCAACACAGACTACACAT 500
Db 477 GACCCCTTCGCTGTAATGATGATTCATCTCTTAACCGTGAAGTAAAGTAAAGATGACAG 536
QY 501 GAACATGATGACATCTACGTTTGGACGCTTATTTGGGCTGTGTGGGCTGTGCT 560
Db 537 AGGCTTCATGACATCCACATTTGGGCGCTTACTTGGGCTACAGAGTACCCGGATCT 596
QY 561 GCCAAGCCTTACCCGAGGAGAGAGATGAATGATGAGACAGACATACCCAGTTT 620

Db 597 CTACGAGCAACCTAGACAGAGAGAGACGAATTTGTGTACCACTGCGACCT 656
QY 621 GTCTGCCATCTGGGCGGCGCTTCTTGTGATGTTCTGGCAAGTTTCAACTGTGCTCT 680
Db 657 CTTTGCCATGATTTGGACACCTCTCTCTGTGATGATGATCTGGCCAGCTTCACTGACCT 716
QY 681 GCTGAGAGTCCAAATCGAAAGAGAAATCCGTGTTCAACACCTTACTATGTGTAGCACT 740
Db 717 ATCTACCAATGGGGAGACGACACAGACCGCCCATCAACACTACTGCTCTCTGGACAG 776
QY 741 CAGCGGTGGACAGCATCTGACAGGTGATCTTGGCTACCCCAAGGGAATATGACGA 800
Db 777 GTGCGCTTCACTCGGTGCAATATTCAGTCCCTTCCACAAAGAGGCACTGACAT 836
QY 801 GACTTATGTACACAGTGGCGGTGGTGGCAGAGAGCGGTGGTGGTACCTGCTGACCT 860
Db 837 GGTGCACTACCAAGATTCACAGCTGCGAGAGAGGGTGGCGGTGACCGTGTGAGAT 896
QY 861 GATCCCTTCCGTGGCTTGCATGATGCTGGGTCTTGTGGCTGGGCTGATCTCGGTGG 920
Db 897 GATGCTCATGCTTACGAGTGGCGCTCATATTCATGCTGCTGCGCATCATCTCACACT 956
QY 921 GGGAGCAAGTACCTGCGGGGTGTGTACCGAGTGTGGGGATTTCCCAAGCTCCAT 980
Db 957 GGGTTTGTATACCTGACCCCATTCCTGTGAGTCCGCGTGCATTCACAGACATGTGG 1016
QY 981 CATGGGCTACACTTCACTGCTGCTGGTCTGCTTGGAGATCATCTACATGTG 1035
Db 1017 CATTAACATCTGCAATGCGATTCCTGCGCATCATATGAGGCGCATGTGGGTGCTGTG 1071

RESULT 3
US-09-949-145-1
; Sequence 1, Application US/0949145
; Patent No. US20020055622A1
; GENERAL INFORMATION:
; APPLICANT: New York Blood Center
; TITLE OF INVENTION: Mammalian No. US20020055622A1-erythroid Rh Type C Genes and G
; FILE REFERENCE: Docket 454-31
; CURRENT APPLICATION NUMBER: US/09/949,145
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/230660
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1952
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION: AF193809
; DATABASE ACCESSION NUMBER: AF193809
; DATABASE ENTRY DATE: 1999-12-22
; RELEVANT RESIDUES: (1)..(1952)
US-09-949-145-1

Query Match 13.2%; Score 165.4; DB 9; Length 1952;
Best Local Similarity 49.1%; Pred. No. 2.9e-42;
Matches 439; Conservative 0; Mismatches 456; Indels 0; Gaps 0;

QY 141 CTAATCAAGTTGGCCAAAGATCTGACCGTGTATGGCGGCCATTTGGCTTGGGCTTCTACCTC 200
Db 201 CTACCCAAAGCTTCCAGAGACGTGATGCTTCTGCGGCTTCCGCTTCTCATATGAC 260
QY 201 GAGTTTCGGAGACAGCTGAGAGTGTATCACTAATATCTTCAACCTTCCATGCTGGCGCTTGG 260
Db 261 TTTCCTGACGCGCTTACGCGCTTCAAGCGCGTGGGCTTCAACCTTCTGTTGGACGCTTTCGG 320
QY 261 TGTGAGTGGGCAATCTGCTGAGAGGCTTCTGAGCCAGTTCCTTCTGGGAAGGTGT 320
Db 321 CATCCAGTGGGCGGTGCTATGACAGGCTGTTCCACTTCTTACAAGACCGCTACATCTGT 380
QY 321 CATCAACTGTTCAATATGCTGCTGCGCCACCATGATGCTTGTGCGGTGCTGATCTCACT 380


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; PRIOR APPLICATION NUMBER: US 60/230660
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: AF193810
; DATABASE ENTRY DATE: 1999-12-22
; RELEVANT RESIDUES: (1)..(2097)
US-09-949-145-2

Query Match      12.0%; Score 150.2; DB 9; Length 2097;
Best Local Similarity 47.5%; Pred. No. 2.4e-37;
Matches 446; Conservative 0; Mismatches 493; Indels 0; Gaps 0;

QY  97 CACTATGACGCTTCCCTTAAGCATCAAAAGGGGCTGTGGCATCTATCAAGTTGGCCAA 156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  258 CCGAAGAACATCTCCAGCGCATGTGAAGAGATTACTATCGCTACCCGAGCTTCCAG 317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  157 GATCTGACCGGTGATGGCGGCATTTGGCTTGGCTTCCACCTCGAGTTTCCGGAGACAC 216
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  318 GATGTAACGCCATGCTCTTCTGGCTTGGCTTCTCTATGACCTTCTCGAGCGCTAC 377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  217 AGCTGAGCAGTGTGGCTTCAACCTTTCATGTGGCGCTTGTGTGCGATGGGCAATC 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  378 GGCTTCAGCGCTGTAGGCTTCAACTCCGTGGCAGCTTGGGCAATCCAGGGGCGACG 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  277 CTGCTGAGCGGCTTCTGAGCCAGTTCCTTCTGGAGAGGTGTATCACTGTTCACT 336
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  438 CTCATGACAGGAGATGTTCCATTACTTTGAAGAGGCCAATGTCTCTGAGCGTCGAGAAC 497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  337 ATTGGCTGGCCACCATGATGCTTGTGGTGTGATGTCACTGATGATGCTGCTGGG 396
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  498 ATCATTCAGAGTACTTCTGTGTGGCATTTCTCTGTGTGGCTTCTGGGCGAGTTTACG 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  397 AAGGTCAACTTGGCGCAGTGTGTGATGTGTGGTGTGGAGAGTGAACACTTGAAGCAAC 456
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  558 AAGGTACGCCCATGAGCTGCTCATTAATGACCTTCTCCAGTGAATGATCTCTACAGATG 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  457 CTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 516
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  618 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  517 TACGTTTGGCAGCACTATTTGGGCTGTGTGGCTGTGGCTGTGGCAAGCCTGACCC 576
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  678 CACACATTTGGGCGCTACTTTGGGCTCACAGTGAATGATGATGATGATGATGATGATG 737
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  577 GAGGGAACGAGAGATTAAGATCAGACAGCAACGATACCCAGTTTGTCTGCCATGTCTGG 636
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  738 GATCAGAGCAGACAGACAGACAGCTGATGATGATGATGATGATGATGATGATGATG 797
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  637 GCGCTCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 696
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  798 ACCCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 857
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  697 GAAAGAGATAGCCGTTTAAACACCTTATGCTGATGCTGATGCTGATGCTGATGCTG 756
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  858 GCCCAGACACCGAGACCCCTCAATACCTACTCTCTTGGCAGCGATGTGCTAACACAA 917
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  757 ATCTGAGGTCATCTTGGCTCAGCCCAAGGAGAGATCAGCAAGATGATGATGATGATG 816
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  918 GTGACAGATTCAGATATGTACAAAGGAGAGATGATGATGATGATGATGATGATGATG 977
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  817 GCGGTGTGTGAGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 876
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  978 GCGAGCTGTGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1037
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  877 CTGCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 936
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  1038 GCGGCTCTCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1097
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

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QY  937 CCGGGCTGTGTAAACGAGTGTGGGATTTCCACAGCTCATATGAGGCTACAACTTC 996
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  1098 ACCGATCTCTGAGAGTCCCGCTTGCATTCACAGACATGTGGCATTTGCAACCTGCAC 1157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  997 AGCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1035
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  1158 GGCATTCGTGGCATATAGCGGCAATGTGGTGTGTGTGTGTGTGTGTGTGTGTGT 1196
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-10-027-632-282039
; Sequence 282039, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 282039
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-282039

Query Match      11.5%; Score 144.6; DB 13; Length 505;
Best Local Similarity 86.9%; Pred. No. 7.1e-36;
Matches 159; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY  758 TCTCAGGAGTCACTTGGCTACCCCAAGGAGATCAGCAAGTATGATGACAGTG 817
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  241 TCTCTCTACTCTTCTTCTTACCCACAGCTATTTCTTGCAGACTTATGTGACAGTG 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  818 CGGTGTGGCAGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 877
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  301 CGGTGTGGCAGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  878 TTGCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 937
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  361 TTGCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  938 GGG 940
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  421 CGG 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-10-027-632-282040
; Sequence 282040, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
```

```
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 282040
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-282040
```

```
Query Match 11.5%; Score 144.6; DB 13; Length 505;
Best Local Similarity 86.9%; Pred. No. 7.1e-36;
Matches 159; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
```

```
OY 758 TCTCAGGGTCATCTTGGCTCACCCCAAGGAGATGACGACGATGTCACAGTG 817
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 241 TCTCTACCTCTTCTCTTCTTACCCACAGCATTTCTTGGACGATGTCACAGTG 300
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
OY 818 CGGTGTGGCAGAGAGCGGTGGCTGTGGTACCTGTGACCTGATCCCTTCCGTGGC 877
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 301 CGGTGTGGCAGAGAGCGGTGGCTGTGGTACCTGTGACCTGATCCCTTCCGTGGC 360
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
OY 878 TTGCATGTGTGCTGGGTCTTGTGGCTGGGCTGATCTCCGTGGGGAGCCAAATACCTGC 937
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 361 TTGCATGTGTGCTGGGTCTTGTGGCTGGGCTGATCTCCGTGGGGAGCCAAATACCTGC 420
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
OY 938 CGG 940
    |||
Db 421 CGG 423
```

```
RESULT 8
US-10-027-632-282041
; Sequence 282041, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 282041
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Human
```

US-10-027-632-282041

```
Query Match 11.5%; Score 144.2; DB 13; Length 505;
Best Local Similarity 86.3%; Pred. No. 9.5e-36;
Matches 158; Conservative 1; Mismatches 24; Indels 0; Gaps 0;
```

```
OY 758 TCTCAGGGTCATCTTGGCTCACCCCAAGGAGATGACGACGATGTCACAGTG 817
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 241 TCTCTACCTCTTCTCTTCTTACCCACAGCATTTCTTGGACGATGTCACAGTG 300
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
OY 818 CGGTGTGGCAGAGAGCGGTGGCTGTGGTACCTGTGACCTGATCCCTTCCGTGGC 877
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 301 CGGTGTGGCAGAGAGCGGTGGCTGTGGTACCTGTGACCTGATCCCTTCCGTGGC 360
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
OY 878 TTGCATGTGTGCTGGGTCTTGTGGCTGGGCTGATCTCCGTGGGGAGCCAAATACCTGC 937
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 361 TTGCATGTGTGCTGGGTCTTGTGGCTGGGCTGATCTCCGTGGGGAGCCAAATACCTGC 420
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
OY 938 CGG 940
    |||
Db 421 CGG 423
```

```
RESULT 9
US-10-027-632-282042
; Sequence 282042, Application US/10027632
; GENERAL INFORMATION:
```

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 282042
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-282042
```

```
Query Match 11.5%; Score 144.2; DB 13; Length 505;
Best Local Similarity 86.3%; Pred. No. 9.5e-36;
Matches 158; Conservative 1; Mismatches 24; Indels 0; Gaps 0;
```

```
OY 758 TCTCAGGGTCATCTTGGCTCACCCCAAGGAGATGACGACGATGTCACAGTG 817
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 241 TCTCTACCTCTTCTCTTCTTACCCACAGCATTTCTTGGACGATGTCACAGTG 300
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
OY 818 CGGTGTGGCAGAGAGCGGTGGCTGTGGTACCTGTGACCTGATCCCTTCCGTGGC 877
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 301 CGGTGTGGCAGAGAGCGGTGGCTGTGGTACCTGTGACCTGATCCCTTCCGTGGC 360
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
OY 878 TTGCATGTGTGCTGGGTCTTGTGGCTGGGCTGATCTCCGTGGGGAGCCAAATACCTGC 937
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 361 TTGCATGTGTGCTGGGTCTTGTGGCTGGGCTGATCTCCGTGGGGAGCCAAATACCTGC 420
    |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
OY 938 CGG 940
    |||
```



```

: Patent No. US20020048763A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Penn, Sharron G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
: FILE REFERENCE: Aecmics-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 18306
:
: LENGTH: 123
: TYPE: DNA
: ORGANISM: Homo sapiens
:
: FEATURE:
: OTHER INFORMATION: MAP TO AL031284.9
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
: OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
: OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.5
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
: OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 2.5
: OTHER INFORMATION: NT HIT: g11139304, EVALUE 2.00e-63
: OTHER INFORMATION: SWISSPROT HIT: P18577, EVALUE 2.00e-20
: OTHER INFORMATION: EST_HUMAN HIT: T84327.1, EVALUE 3.00e-53
:
: US-09-864-761-18306

```

OY		487	ACAGCTCCACATTAACATGATGTGAACAATCACTCGATTGGCAGCCTAATTTGGGCTGT	546
Dd		123	ACAGCTACCATATGAACCTTGGGCAGCTTTCTTAGTGTTTCGAGCCTAATTTTGGGCTACT	64
OY		547	GTCGCTGTGTGCTGTGCCAAAGCCTTCTACCOCGAGGAGACGAGATTAAGATCAGAACGA	606
Dd		63	GTCGCTGTGTGCTGTGCCAAAGCCTTCTACCOCGAGGAGACGAGATTAAGATCAGAACGA	4
OY		607	ACG 609 	
Dd		3	ACG 1	
RESULT 13				
US-10-012-542-75				
; Sequence 75, Application US/10012542				
; Publication No. US20030044851A1				
GENERAL INFORMATION:				
APPLICANT: Ruben et al.				
TITLE OF INVENTION: 94 Human Secreted Proteins				
FILE REFERENCE: PZ029P1				
CURRENT APPLICATION NUMBER: US/10/012,542				
PRIOR FILING DATE: 2001-12-12				
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325				
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14				
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507				
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16				
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508				
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16				
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509				
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16				
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510				
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16				
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112				
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22				
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113				
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22				
NUMBER OF SEQ ID NOS: 532				
SOFTWARE: Patentin Ver. 2.0				
SEQ ID NO: 75				
LENGTH: 1650				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-10-012-542-75				
Query Match 8.7%; Score 109.6; DB 14; Length 1650;				
Best Local Similarity 48.7%; Pred. 2..7e-24;				
Matches 327; Conservative 0; Mismatches 344; Indels 1; Gaps 1				
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Dd		33	TCGTCTCGCGTGCCCTTTGGGGCAATTTCTGGGTAAAGTAGGCCCACTTAGCTGCTCATC	92
OY		424	ATGTGCTGTGTGAGAGTGACAGCTTTAGGCAACCTGAGAGATGTCATCAGTATAATCTTC	483
Dd		93	ATGACTTTCTTCCAAGTGAACCTCTTCGCTGTGAATGAATCATCTCTCTTAACCTGCTA	152
OY		484	AACACAGACTACCACATATGAACTATGACATCTACGTGTGTGCAAGCCTAATTTGGGCTG	543
Dd		153	AAGGTGAAGATGACGAGAGGCTCCATGACCATCCACATTTTGGGCGCCATCTTGGGCTC	212
OY		544	TCTGTGGCGTGTGCTGCGCCAAAGCCTCTACCCGAGAGGAGGAGAGATTAAGATCAGACA	603
Dd		213	ACAGTGACCCGATCTCTCTACGAGCAACCTTAGACAGAGACGAAGAGACAGAAATTTCT	272
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Dd		273	GTGTACCAAGTGCGACCTCTTTSCCANMATTTGGCACACCTCTCTCTGTGATGTACTGGCCC	332
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Dd		333	AGCTTCAACTCAGCCATATCTTACCATGGGAGACACGACGAGCCGACCATCAAACACC	392

OY	481	TTCAACAGACGCTACACATGATATGACATTCACATCGTTGCGAGCCTATTATTTGGG	540
Db	508	TTCAACAGACGCTACACATGATATGACATTCACATCGTTGCGAGCCTATTATTTGGG	567
OY	541	CTGTCTGTGCGCTGGTGCCTGCACAAAGCGCTTACCCGAGGAGGAGATAAAGATCAG	600
Db	568	CTGACGTGCGCTGGTGCCTGCACAAAGCGCTTACCCGAGGAGGAGATAAAGATCAG	627
OY	601	ACAGCAGCATACCCAGTTTGTCTTGCCATGCTGGGCGCCCTCTCTTGT	649
Db	628	AGAGCAGCATACCCAGTTTGTCTTGCCATGCTGGGCGCCCTCTCTTGT	676
RESULT 4			
LOCUS	B0655978	685 bp	linear
DEFINITION			EST 30-SEP-2002
ACCESSION	B0655978		
VERSION	B0655978.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 685)		
AUTHORS	Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.		
TITLE	Gene Expression in Human Erythroid Precursor Cells		
JOURNAL	Unpublished		
COMMENT	Contact: Jeffery L. Miller Laboratory of Chemical Biology National Institute of Diabetes and Digestive and Kidney Diseases Building 10, Room 9B17, National Institutes of Health, Bethesda, MD 20892, USA Tel: 301 402 2373 Fax: 301 435 5148 Email: jml7f@nih.gov The 'cl' library was constructed by Alexander Gubin, Ph.D. in the Laboratory of Chemical Biology, NIDDK, NIH. DNA sequencing and/or analyses by National Institutes of Health Intramural Sequencing Center (NISC). More information available at: http://hembase.niddk.nih.gov Plate: 04 row: 9 column: 11 Seq primer: 5' lambda-Triplex2 Sequencing Primer. Location/Qualifiers		
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	/note="Organ: Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI; A complementary DNA (cDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA Library Construction Kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 umol/L peptide nucleic acid (PNA) oligos (N-terminal)-blotin-GTC-CAC-CGC-AAG-CYT-G-(C-terminal) and (N-terminal) biotin-C(T/C)T-GAA-GMT-CTC-AGG-A-(C-terminal). Synthesized cDNA was digested with SfiI and size selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH		

	Intramural Sequencing Center (INSC); Http://www.nisc.nih.gov/).
BASE COUNT	129 a 183 c 200 g 173 t
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Query Match	49.2%; Score 617.2; DB 13; Length 685;
Best Local Similarity	98.0%; Pred.No. 4,8e-151;
Matches 625; Conservative	0; Mismatches 13; Indels 0; Gaps 0
OY	1 ATGAGCTCTAAGTATACCCGGCTGTCTCCGGCGCTCCTGCCCTTTGGGCCCTTAACACTG 60
Db	48 ATGAGCTCTAAGTATACCCGGCGGTCTTTGGGGCTCCGGCCCTTGCGGCCTTAACACTG 107
OY	61 GAAGCACTCTTCATTCTCTCTCTTCTAATTTTTTACCACATAGACGCTTCTTAGAGAT 120
Db	108 GAAGCACTCATCTCTCTCTCTTCTAATTTTTTACCACATAGACGCTTCTTAGAGAT 167
OY	121 CAAAGGGGGCTGTGGGCAATCTATCAATTTGGCCAAAGATCTGACCGTATGGGGCCATT 180
Db	168 CAAAAGGGGGCTGTGGGCAATCTATCAATTTGGCCAAAGATCTGACCGTATGGGGCCATT 227
OY	181 GGCTTGGGCTTCTCACCTCGAGTTTCGGAGACACACTGAGACAGTGTGGCTTTCAC 240
Db	228 GGCTTGGGCTTCTCACCTCGAGTTTCGGAGACACACTGAGACAGTGTGGCTTTCAC 287
OY	241 CTCTTCATGCTGGCGCTTGTGTGCAGTGGGCAATCTGCTGGACGGCTTCTGAGCCAG 300
Db	288 CTCTTCATGCTGGCGCTTGTGTGCAGTGGGCAATCTGCTGGACGGCTTCTGAGCCAG 347
OY	301 TTCCCTTTGGGGAAGGTGGTATCATCACTGTTTCACTATTGGCGTGGCCACCATGAGTCT 360
Db	348 TTCCCTTTGGGGAAGGTGGTATCATCACTGTTTCACTATTGGCGTGGCCACCATGAGTCT 407
OY	361 TTGTGCGGTGATCTCAGTGATGCTCTCTTGGGGAAGTCACTTGGCCAGTTGGTG 420
Db	408 GTGTGCGGTGATCTCAGTGATGCTCTCTTGGGGAAGTCACTTGGCCAGTTGGTG 467
OY	421 GTGATGTGTGTGGTGGAGGTGACAGCTTTAAGGCAACTGTAGAGANGTCATGATAATATC 480
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OY	481 TTCAACAACAGACTACCAATATGAATGATGACATCTACGTGTTCCGACGCTATTTTGG 540
Db	528 TTCAACAACAGACTACCAATATGAATGATGACATCTACGTGTTCCGACGCTATTTTGG 587
OY	541 CTGTCTGTGGCGCTGGTGCCTGCCAAAGGCTCTACCCGAGGGAACGAGATAAAGATCAG 600
Db	588 CTGACTGTGGCGCTGGTGCCTGCCCAAAGGCTCTACCCAAAGGGAACGAGATAAAGATCAG 647
OY	601 ACAGCAACGATACCCAGTTTGTCTGCCATGCTGGGGCG 638
Db	648 AGAGCAACGATACCCAGTTTGTCTGCCATGCTGGGGCG 685
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LOCUS	BX406634 Homo sapiens FETAL LIVER Homo sapiens cdna clone
DEFINITION	CDSMDM13YA17 3-PRIME, mRNA sequence.
ACCESSION	BX406634
VERSION	BX406634.1 GI:30656378
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1.(bases 1 to 1000) L1,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cdna libraries and normalization Unpublished Contact: Genoscope Genoscope - Centre National de Sequencage BP 19191006 Evry cedex - France

TITLE and Hayashizaki, Y.
JOURNAL Functional annotation of a full-length mouse cDNA collection
MEDLINE Nature 409 (6821), 685-690 (2001)
PUBMED 21085660
11217851

REFERENCE
5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1457)

AUTHORS Adachi, T., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagata, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.
location/Qualifiers

FEATURES
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Best Local Similarity 69.7%; Pred. No. 5,6e-147;
Matches 884; Conservative 0; Mismatches 358; Indels 27; Gaps 4;

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DB 607 ACAAGATACCAAGTGTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCG 666
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			Gaps 0	
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Db	84	ATGAGCGCTAAGTACCGCGGGGTGTCGCGCGGCGCTGCGCCCTGCGGGCCCTTAACACTG	143	
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Db	144	GAAGCAGCTGCATCTCTCTCTCTATTTTTTACCACATAGACGGCTTCCTTAGAGAT	203	
QY	121	CAAAAGGGGCTCGTGGCATCCTATCAAGTTGGCCAGATCTGACCGTGATGGCGCCATT	180	
Db	204	CAAAAGGGGCTCGTGGCATCCTATCAAGTTGGCCAGATCTGACCGTGATGGCGCCATT	263	
QY	181	GGCTGTGGGCTTCCACACCTGAGATTTCCGGAGACACACAGCTGGAGCATGTGGCTTAAAC	240	
Db	264	GGCTGTGGGCTTCCACACCTGAGATTTCCGGAGAGACACAGCTGGAGCATGTGGCTTAAAC	323	
QY	241	CTCTTCATGCTGGGCGCTTGGTGTGCACTGGGCAATCCTGCTGACAGGCTTCTAGACCAAG	300	
Db	324	CTCTTCATGCTGGGCGCTTGGTGTGCACTGGGCAATCCTGCTGACAGGCTTCTAGACCAAG	383	
QY	301	TTCCCTTGGGGAAGGTGTATCATCACTGTTCAATTCGAGTGGCTGGCCACCATGAGTCT	360	
Db	384	TTCCCTTGGGGAAGGTGTATCATCACTGTTCAATTCGAGTGGCTGGCCACCATGAGTCT	443	
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QY	421	GTCATGTGTGCTGTGAGAGTGCACGCTTAGAGCAACCTGAGAGTGTATCAGTAATATC	480	
Db	504	GTCATGTGTGCTGTGAGAGTGCACGCTTAGAGCAACCTGAGAGTGTATCAGTAATATC	563	
QY	481	TTCAACACAGACTACACATGATGATGACATCTACGTTTCGAGCCCTAATTTTGGG	540	
Db	564	TTCAACACAGACTACACATGATGATGACATCTACGTTTCGAGCCCTAATTTTGGG	623	
QY	541	CTGCTGTGTGGCGCTGTGCTGCCCAAAAGCCTTACCAGAGGAAACGAGAGTAAGAATCAG	600	
Db	624	CTGCTGTGTGGCGCTGTGCTGCCCAAAAGCCTTACCAGAGGAAACGAGAGTAAGAATCAG	683	
QY	601	ACAGCAACGATATCCAGTTTGTG	623	
Db	684	AGAGCAACGATATCCAGTTTGTG	706	

RESULT 8

B0662207

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

B0662207

c182h04.21

B0662207

B0662207.1

EST

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

631 bp

mRNA

Linear

EST 30-SEP-2002

cl82h04.21 Hembase; Erythroid Precursor Cells (LCB:cl library) Homo

sapiens cDNA clone c182h04.5, mRNA sequence.

GI:23374389

Homo sapiens (human)

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 631)
 AUTHORS Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.
 TITLE Gene Expression in Human Erythroid Precursor Cells
 JOURNAL Unpublished
 COMMENT Contact: Jeffery L. Miller
 Laboratory of Chemical Biology
 National Institute of Diabetes and Digestive and Kidney Diseases
 Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
 20892, USA
 Tel: 301 402 2373
 Fax: 301 435 5148
 Email: jml7@nih.gov

The 'cl' library was constructed by Alexander Gubin, Ph.D. in the Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or analyses by National Institutes of Health Intramural Sequencing Center (NISC). More information available at:
<http://hembase.nidk.nih.gov>
 Plate: 82 row: h column: 04
 Seq primer: 5' lambda-TripLex2 Sequencing primer.
 Location/Qualifiers

FEATURES

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 /clone_lib="Hembase; Erythroid Precursor Cells (LCB:cl library)"
 /note="Organ: blood; Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI. A complementary DNA (cDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA Library Construction Kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 umol/L peptide nucleic acid (PNA) oligos (N-terminal)-biotin-6TC-CAC-CCG-AGG-CTT-6-(C-terminal) and (N-terminal)-biotin-C/T/C/T-GAA-GTT-CTC-AGG-A-(C-terminal) . Synthesized cDNA was digested with SfiI and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC).
[Http://www.nisc.nih.gov/](http://www.nisc.nih.gov/)."

BASE COUNT 114 a 163 c 188 g 165 t 1 others

Query Match 44.7%; Score 560.4; DB 13; Length 631;
 Best Local Similarity 99.6%; Pred. No 3.9e-136;
 Matches 561; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATAGCTCTAAGTACCGCGGCTGTCCGCGCTGCTGCTGCTGCGCTTACACTG 60
 Db 69 ATAGCTCTAAGTACCGCGGCTGTCCGCGCTGCTGCTGCGCTTACACTG 128
 QY 61 GAAGCAGCTCTATTCTCTCTTCTATTTTATTTTACCACATAGACGCTTCTTAGAGAT 120
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 Db 189 CAAAGGGGCTGCTGCATCTATCAAGTTGGCAAGATGTGACCGTGATGGGGCATT 248
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 Db 249 GCGTTGGGCTTCTCCTACCTGAGTTTCCGAGACACAGCTGAGAGTGTGGCTTCAAC 308

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 QY 301 TTCCCTTCTGGGAAGGTGCTATCAGCTGTTCAGTATTTGGCTGGCCACCATTAGTGT 360
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 QY 541 CTGCTGTGGCTGCTGCTGCTGCC 563
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RESULT 9

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES
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 /note="Organ: blood; Vector: pTriplex2; Site_1: SfiI;

Site_2: SfiI; A complementary DNA (cDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA library construction kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 umol/L peptide nucleic acid (PNA) oligos (N-terminal (N-terminal)-biotin-CAC-CCG-AGG-CTT-G-(C-terminal) and (N-terminal)-biotin-C(T/C)-T-GAA-GTT-CTC-AGG-A-(C-terminal). Synthesized cDNA was digested with SfiI and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC); <http://www.nisc.nih.gov/>.

BASE COUNT 115 a 171 c 185 g 161 t
ORIGIN

Query Match 44.6%; Score 559; DB 13; Length 632;
Best Local Similarity 98.3%; Pred. No. 9e-136;
Matches 565; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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RESULT 10

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VERSION BU664659.1 GI:23376845
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 613)
AUTHORS Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.
TITLE Gene Expression in Human Erythroid Precursor Cells
JOURNAL Unpublished
COMMENT

Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD 20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jm7feinh.gov
The 'cl' library was constructed by Alexander Gubin, Ph.D. in the Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or analyses by National Institutes of Health Intramural Sequencing Center (NISC). More information available at: <http://hembase.nidk.nih.gov>
Plate: 120 row: e column: 10
Seq primer: 5' lambda-Triplex2 Sequencing Primer.

FEATURES

source

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/note="Organ: blood; Vector: pTriplex2; site_1: SfiI; site_2: SfiI; A complementary DNA (cDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA library construction kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 umol/L peptide nucleic acid (PNA) oligos (N-terminal (N-terminal)-biotin-CAC-CCG-AGG-CTT-G-(C-terminal) and (N-terminal)-biotin-C(T/C)-T-GAA-GTT-CTC-AGG-A-(C-terminal). Synthesized cDNA was digested with SfiI and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC); <http://www.nisc.nih.gov/>."

BASE COUNT 110 a 159 c 181 g 161 t 2 others
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FEATURES

KEYWORDS HTC; CAP trapper.

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Konno, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, M., Gaasterland, T., Gissi, C., King, B., Koichiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staudli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carlini, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-oka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	6 (bases 1 to 975)
PUBMED	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaka, J., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Konno, S., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sobge, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

TITLE	Muramatsu, M. and Hayashizaki, Y.
JOURNAL	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers
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 1 (bases 1 to 587)
 Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.
 Gene Expression in Human Erythroid Precursor Cells
 Unpublished
 CONTACT: Jeffery L. Miller
 Laboratory of Chemical Biology
 National Institute of Diabetes and Digestive and Kidney Diseases
 Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
 20892, USA
 Tel: 301 402 2373
 Fax: 301 435 5148
 Email: jmlfe@nih.gov
 The 'cl' library was constructed by Alexander Gubin, Ph.D. in the
 Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or
 analyses by National Institutes of Health Intramural Sequencing
 Center (NISC). More information available at:
 http://hembase.nidk.nih.gov
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 construction kit (Clontech, Palo Alto, CA) according to
 the manufacturer's directions, but with slight
 modifications. Briefly, reverse transcription was
 performed in the presence of 1 umol/L peptide nucleic acid
 (PNA) oligos (N-terminal
)-biotin-GTC-CAC-CCG-AAG-CTT-G-(C-terminal) and
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). Synthesized cDNA was digested with SfiI and
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 ACCESSION B0659596
 VERSION B0659596.1 GI:23371778
 KEYWORDS EST.
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 480)
 Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.
 Gene Expression in Human Erythroid Precursor Cells
 Unpublished
 CONTACT: Jeffery L. Miller
 Laboratory of Chemical Biology
 National Institute of Diabetes and Digestive and Kidney Diseases
 Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
 20892, USA
 Tel: 301 402 2373
 Fax: 301 435 5148
 Email: jmlfe@nih.gov
 The 'cl' library was constructed by Alexander Gubin, Ph.D. in the
 Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or
 analyses by National Institutes of Health Intramural Sequencing
 Center (NISC). More information available at:

http://hembase.nidk.nih.gov
Plate: 49 row: f column: 09
Seq primer: 5' lambda-TripLex2 Sequencing Primer.
Location/Qualifiers
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FEATURES
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Query Match 31.8%; Score 399.2; DB 13; Length 480;
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Matches 404; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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